

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 9, 2004, 23:42:43 ; Search time 31 Seconds  
(without alignment)  
6.661 Million cell updates/sec

Title: US-10-076-071-1

Perfect score: 23

Sequence: 1 DAHX 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1000 summaries

Database : Issued Patents AA:\*  
1: /cgn2\_6/prodata/2/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/2/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/2/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/2/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/2/iaa/PTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	4	4	US-09-165-926-1
2	23	100.0	4	4	US-09-165-961-1
3	23	100.0	4	4	US-09-165-581-1
4	23	100.0	6	1	US-08-469-856-10
5	23	100.0	8	4	US-09-165-926-2
6	23	100.0	8	4	US-09-165-961-2
7	23	100.0	8	4	US-09-165-581-2
8	23	100.0	11	1	US-08-469-856-9
9	23	100.0	24	2	US-08-702-572-13
10	23	100.0	28	4	US-09-846-329A-1
11	23	100.0	42	4	US-09-480-993-19
12	23	100.0	68	4	US-09-134-000C-4709
13	23	100.0	134	4	US-09-615-192A-316
14	23	100.0	138	4	US-09-134-001C-4838
15	23	100.0	144	4	US-09-328-352-7792
16	23	100.0	168	4	US-09-325-932A-69
17	23	100.0	172	4	US-08-858-207A-499
18	23	100.0	174	2	US-08-683-262B-41
19	23	100.0	174	3	US-09-361-707-41
20	23	100.0	174	4	US-09-134-000C-6037
21	23	100.0	175	4	US-09-328-352-7480
22	23	100.0	175	4	US-09-134-000C-4705
23	23	100.0	183	4	US-09-540-236-3135
24	23	100.0	187	4	US-09-543-681A-4322
25	23	100.0	195	4	US-09-328-352-8131
26	23	100.0	196	4	US-08-679-493A-185
27	23	100.0	200	4	US-09-107-532A-4207

28	23	100.0	201	4	US-09-134-000C-6503	Sequence 6503, Ap
29	23	100.0	207	1	US-07-656-566-2	Sequence 2, Appli
30	23	100.0	211	4	US-09-134-000C-3723	Sequence 3723, Ap
31	23	100.0	211	4	US-09-134-000C-5067	Sequence 5067, Ap
32	23	100.0	213	4	US-09-134-000C-4335	Sequence 4335, Ap
33	23	100.0	214	4	US-09-134-000C-4529	Sequence 4529, Ap
34	23	100.0	218	4	US-09-328-352-4385	Sequence 4385, Ap
35	23	100.0	227	4	US-09-328-352-4162	Sequence 4162, Ap
36	23	100.0	231	1	US-07-656-566-3	Sequence 3, Appli
37	23	100.0	231	3	US-08-721-259-2	Sequence 2, Appli
38	23	100.0	231	4	US-09-611-216-2	Sequence 2, Appli
39	23	100.0	231	4	US-10-386-972-2	Sequence 2, Appli
40	23	100.0	243	4	US-09-252-991A-29411	Sequence 29411, A
41	23	100.0	255	4	US-09-252-991A-31162	Sequence 31162, A
42	23	100.0	270	4	US-09-252-991A-16842	Sequence 16842, A
43	23	100.0	271	4	US-09-252-991A-19255	Sequence 19255, A
44	23	100.0	271	4	US-09-328-352-7066	Sequence 7066, Ap
45	23	100.0	274	2	US-07-857-224B-29	Sequence 29, Appl
46	23	100.0	276	4	US-09-660-587-44	Sequence 44, Appl
47	23	100.0	276	4	US-09-314-701-42	Sequence 42, Appl
48	23	100.0	276	4	US-09-811-007A-44	Sequence 44, Appl
49	23	100.0	277	2	US-08-147-784-2	Sequence 2, Appli
50	23	100.0	277	3	US-08-195-967-2	Sequence 2, Appli
51	23	100.0	277	3	US-09-006-353A-12	Sequence 12, Appl
52	23	100.0	277	3	US-08-472-940-2	Sequence 2, Appli
53	23	100.0	277	4	US-09-573-986-12	Sequence 12, Appl
54	23	100.0	277	4	US-09-880-939-2	Sequence 2, Appli
55	23	100.0	277	4	US-09-804-200-2	Sequence 2, Appli
56	23	100.0	277	4	US-08-469-633A-4	Sequence 4, Appli
57	23	100.0	277	4	US-09-107-532A-4676	Sequence 4676, Ap
58	23	100.0	280	3	US-08-953-326-17	Sequence 17, Appl
59	23	100.0	280	4	US-09-660-587-14	Sequence 14, Appl
60	23	100.0	280	4	US-09-261-358A-14	Sequence 14, Appl
61	23	100.0	280	4	US-09-201-458-10	Sequence 10, Appl
62	23	100.0	280	4	US-09-314-701-12	Sequence 12, Appl
63	23	100.0	280	4	US-09-553-663-17	Sequence 17, Appl
64	23	100.0	280	4	US-10-062-994-17	Sequence 17, Appl
65	23	100.0	280	4	US-09-811-007A-14	Sequence 14, Appl
66	23	100.0	286	3	US-09-120-365-78	Sequence 78, Appl
67	23	100.0	286	3	US-09-515-039-78	Sequence 78, Appl
68	23	100.0	288	4	US-09-314-701-32	Sequence 32, Appl
69	23	100.0	295	4	US-09-489-039A-9641	Sequence 9641, Ap
70	23	100.0	298	2	US-08-061-636-3	Sequence 3, Appli
71	23	100.0	298	2	US-08-874-347-19	Sequence 19, Appl
72	23	100.0	298	3	US-09-093-522-19	Sequence 19, Appl
73	23	100.0	298	5	PCT-US94-05268-3	Sequence 3, Appli
74	23	100.0	304	4	US-09-543-681A-6103	Sequence 6103, Ap
75	23	100.0	307	4	US-09-543-681A-6403	Sequence 6403, Ap
76	23	100.0	312	4	US-09-107-532A-5684	Sequence 5684, Ap
77	23	100.0	313	4	US-09-540-236-2394	Sequence 2394, Ap
78	23	100.0	337	4	US-09-540-236-3792	Sequence 3792, Ap
79	23	100.0	355	2	US-08-865-203-5	Sequence 5, Appli
80	23	100.0	355	2	US-07-849-420-5	Sequence 5, Appli
81	23	100.0	355	3	US-09-853-854-5	Sequence 5, Appli
82	23	100.0	355	3	US-08-955-424-5	Sequence 5, Appli
83	23	100.0	373	4	US-09-134-000C-4057	Sequence 4057, Ap
84	23	100.0	375	4	US-09-134-001C-3918	Sequence 3918, Ap
85	23	100.0	400	4	US-09-107-532A-4672	Sequence 4672, Ap
86	23	100.0	400	4	US-09-107-532A-4673	Sequence 4673, Ap
87	23	100.0	400	4	US-09-107-532A-4675	Sequence 4675, Ap
88	23	100.0	400	4	US-09-134-000C-5837	Sequence 5837, Ap
89	23	100.0	400	4	US-09-134-000C-6331	Sequence 6331, Ap
90	23	100.0	400	4	US-09-107-532A-6966	Sequence 6966, Ap
91	23	100.0	411	4	US-09-134-001C-2891	Sequence 2891, Ap
92	23	100.0	413	4	US-09-134-001C-3361	Sequence 3361, Ap
93	23	100.0	413	4	US-09-134-001C-4058	Sequence 4058, Ap
94	23	100.0	413	4	US-09-134-001C-4975	Sequence 4975, Ap
95	23	100.0	422	4	US-09-198-452A-1088	Sequence 1088, Ap
96	23	100.0	434	4	US-09-543-681A-7780	Sequence 7780, Ap
97	23	100.0	447	4	US-09-489-039A-8269	Sequence 8269, Ap
98	23	100.0	448	2	US-08-878-989-2	Sequence 2, Appli
99	23	100.0	448	3	US-09-272-796-2	Sequence 2, Appli
100	23	100.0	448	3	US-09-272-796-2	Sequence 2, Appli

101	23	100.0	449	1	US-08-142-439A-5	Sequence 5, Appli	174	4	US-09-107-532A-3716	Sequence 3716, Ap
102	23	100.0	449	2	US-08-869-477-5	Sequence 5, Appli	175	4	US-09-543-681A-7965	Sequence 7965, Ap
103	23	100.0	458	4	US-09-540-236-3313	Sequence 3313, Ap	176	3	US-08-853-160-89	Sequence 8, Appli
104	23	100.0	485	3	US-09-384-212-2	Sequence 2, Appli	177	3	US-10-153-064-89	Sequence 89, Appli
105	23	100.0	488	4	US-09-489-039A-13164	Sequence 13164, A	178	3	US-09-220-641-3	Sequence 3, Appli
106	23	100.0	489	4	US-09-134-001C-2920	Sequence 2920, Ap	179	3	PCT-US94-00198-4	Sequence 4, Appli
107	23	100.0	496	4	US-09-312-762A-15	Sequence 15, Appli	180	3	US-09-134-001C-5080	Sequence 5080, Ap
108	23	100.0	508	3	US-09-344-700-4	Sequence 4, Appli	181	20	US-08-877-605-193	Sequence 193, App
109	23	100.0	508	4	US-09-563-997A-4	Sequence 4, Appli	182	20	US-08-877-605-194	Sequence 194, App
110	23	100.0	510	4	US-09-198-452A-639	Sequence 639, App	183	20	US-09-190-964-13	Sequence 13, Appli
111	23	100.0	514	4	US-09-540-236-3378	Sequence 3178, Ap	184	20	US-07-987-272A-5	Sequence 5, Appli
112	23	100.0	520	1	US-08-708-232-2	Sequence 2, Appli	185	20	US-09-205-258-518	Sequence 518, App
113	23	100.0	520	3	US-09-032-365A-15	Sequence 15, Appli	186	20	US-08-480-473B-45	Sequence 45, Appli
114	23	100.0	521	4	US-09-252-991A-22686	Sequence 22686, A	187	20	US-08-915-213-45	Sequence 45, Appli
115	23	100.0	534	4	US-09-312-762A-4	Sequence 4, Appli	188	20	US-09-205-258-511	Sequence 511, App
116	23	100.0	534	4	US-09-312-762A-5	Sequence 5, Appli	189	20	US-09-205-258-511	Sequence 511, App
117	23	100.0	535	4	US-09-312-762A-10	Sequence 10, Appli	190	20	US-08-311-731A-296	Sequence 296, App
118	23	100.0	535	4	US-09-312-762A-14	Sequence 14, Appli	191	20	US-08-311-731A-296	Sequence 296, App
119	23	100.0	585	1	US-08-153-799-14	Sequence 14, Appli	192	20	US-09-540-236-3270	Sequence 3270, Ap
120	23	100.0	585	2	US-08-448-196A-3	Sequence 3, Appli	193	20	US-09-489-039A-12548	Sequence 12548, A
121	23	100.0	585	2	US-08-984-176-1	Sequence 1, Appli	194	20	US-08-311-731A-296	Sequence 296, App
122	23	100.0	585	2	US-08-702-572-2	Sequence 2, Appli	195	20	US-09-381-122A-26	Sequence 26, Appli
123	23	100.0	585	3	US-08-769-746-2	Sequence 2, Appli	196	20	US-07-987-272A-1	Sequence 1, Appli
124	23	100.0	585	4	US-10-153-064-5	Sequence 5, Appli	197	20	US-09-205-258-730	Sequence 730, App
125	23	100.0	603	1	US-08-222-619-3	Sequence 3, Appli	198	20	US-07-987-272A-14	Sequence 14, Appli
126	23	100.0	609	1	US-08-433-037-4	Sequence 4, Appli	199	20	US-09-107-532A-5880	Sequence 5880, Ap
127	23	100.0	609	4	US-08-897-956A-2	Sequence 2, Appli	200	20	US-08-202-389-20	Sequence 20, Appli
128	23	100.0	609	4	US-10-153-064-7	Sequence 7, Appli	201	20	US-08-529-055-24	Sequence 24, Appli
129	23	100.0	609	4	US-09-976-594-977	Sequence 977, App	202	20	US-08-241-853-11	Sequence 11, Appli
130	23	100.0	609	5	PCT-US95-04075-3	Sequence 3, Appli	203	20	US-08-850-917-11	Sequence 11, Appli
131	23	100.0	610	2	US-08-797-689-2	Sequence 2, Appli	204	20	US-09-621-976-5753	Sequence 5753, Ap
132	23	100.0	610	4	US-09-984-186-2	Sequence 2, Appli	205	20	US-08-846-134-1	Sequence 7197, Ap
133	23	100.0	621	1	US-08-328-961-2	Sequence 2, Appli	206	20	US-09-370-473-10	Sequence 1, Appli
134	23	100.0	621	1	US-08-462-397-2	Sequence 2, Appli	207	20	US-09-010-147B-10	Sequence 10, Appli
135	23	100.0	651	4	US-10-153-064-133	Sequence 133, App	208	20	US-09-134-000C-5247	Sequence 5247, A
136	23	100.0	652	4	US-10-153-064-96	Sequence 96, Appli	209	20	US-09-252-991A-32879	Sequence 32879, A
137	23	100.0	652	4	US-10-153-064-99	Sequence 99, Appli	210	20	US-09-441-340-4	Sequence 10218, A
138	23	100.0	652	4	US-10-153-064-102	Sequence 102, App	211	20	US-08-621-976-7197	Sequence 17439, A
139	23	100.0	652	4	US-10-153-064-105	Sequence 105, App	212	20	US-08-679-006-29	Sequence 6036, Ap
140	23	100.0	653	4	US-10-153-064-132	Sequence 132, App	213	20	US-09-441-340-8	Sequence 4, Appli
141	23	100.0	656	4	US-10-153-064-131	Sequence 131, App	214	20	US-09-441-340-20	Sequence 20, Appli
142	23	100.0	660	4	US-10-153-064-130	Sequence 130, App	215	20	US-09-441-340-26	Sequence 26, Appli
143	23	100.0	660	4	US-10-153-064-90	Sequence 90, App	216	20	US-09-441-340-28	Sequence 28, Appli
144	23	100.0	668	4	US-10-153-064-93	Sequence 93, Appli	217	20	US-09-441-340-30	Sequence 30, Appli
145	23	100.0	676	4	US-10-153-064-95	Sequence 95, Appli	218	20	US-09-441-340-32	Sequence 32, Appli
146	23	100.0	676	4	US-10-153-064-98	Sequence 98, Appli	219	20	US-09-252-991A-22791	Sequence 22791, A
147	23	100.0	676	4	US-10-153-064-104	Sequence 104, App	220	20	US-09-328-352-5004	Sequence 5004, Ap
148	23	100.0	676	4	US-10-153-064-127	Sequence 127, App	221	20	US-09-489-039A-13318	Sequence 13318, A
149	23	100.0	676	4	US-10-153-064-129	Sequence 129, App	222	20	US-09-252-991A-17905	Sequence 17905, A
150	23	100.0	677	4	US-10-153-064-125	Sequence 125, App	223	20	US-09-252-991A-22916	Sequence 22916, A
151	23	100.0	680	4	US-10-153-064-123	Sequence 123, App	224	20	US-09-134-000C-3763	Sequence 3763, Ap
152	23	100.0	684	4	US-10-153-064-92	Sequence 92, Appli	225	20	US-09-252-991A-18043	Sequence 18043, A
153	23	100.0	692	4	US-10-153-064-101	Sequence 101, App	226	20	US-09-205-258-729	Sequence 729, App
154	23	100.0	710	4	US-09-079-8128-2	Sequence 2, Appli	227	20	US-09-489-039A-9043	Sequence 9043, Ap
155	23	100.0	714	4	US-09-828-303-21	Sequence 21, Appli	228	20	US-08-051-142-2	Sequence 2159, Ap
156	23	100.0	720	4	US-09-489-039A-12061	Sequence 12061, A	229	20	US-09-540-236-2159	Sequence 2159, Ap
157	23	100.0	741	4	US-09-543-681A-8128	Sequence 8128, Ap	230	20	US-09-737-248-21	Sequence 21771, A
158	23	100.0	782	4	US-09-540-236-2211	Sequence 2211, Ap	231	20	US-09-252-991A-19168	Sequence 19168, A
159	23	100.0	783	1	US-08-256-938-2	Sequence 2, Appli	232	20	US-08-737-248-18	Sequence 18, Appli
160	23	100.0	787	1	US-08-797-689-16	Sequence 16, Appli	233	20	US-09-489-039A-17057	Sequence 17057, A
161	23	100.0	787	2	US-08-797-689-16	Sequence 16, Appli	234	20	US-08-737-248-20	Sequence 2434, Ap
162	23	100.0	787	4	US-09-984-186-16	Sequence 16, Appli	235	20	US-08-737-248-15	Sequence 15, Appli
163	23	100.0	815	4	US-09-328-352-4284	Sequence 4284, Ap	236	20	US-08-737-248-16	Sequence 16, Appli
164	23	100.0	822	4	US-09-489-039A-8709	Sequence 8709, Ap	237	20	US-08-737-248-17	Sequence 17, Appli
165	23	100.0	849	4	US-09-543-681A-5761	Sequence 5761, Ap	238	20	US-08-737-248-18	Sequence 18, Appli
166	23	100.0	853	4	US-09-254-352B-17	Sequence 17, App	239	20	US-09-252-991A-17057	Sequence 17057, A
167	23	100.0	854	4	US-09-254-352B-18	Sequence 18, Appli	240	20	US-08-737-248-19	Sequence 19, Appli
168	23	100.0	876	4	US-09-254-352B-19	Sequence 19, Appli	241	20	US-09-489-039A-8434	Sequence 8434, Ap
169	23	100.0	883	1	US-08-106-433A-2	Sequence 2, Appli	242	20	US-08-737-248-20	Sequence 20, Appli
170	23	100.0	883	4	US-09-254-352B-16	Sequence 16, Appli	243	20	US-08-737-248-21	Sequence 21, Appli
171	23	100.0	978	4	US-08-897-956A-3	Sequence 3, Appli	244	20	US-08-737-248-22	Sequence 22, Appli
172	23	100.0	1025	2	US-08-530-792D-23	Sequence 23, Appli	245	20		
173	23	100.0	1026	2	US-08-530-792D-22	Sequence 22, Appli	246	20		

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248	20	87.0	199	3	US-08-737-248-5	Sequence 5, Appli	321	20	87.0	279	4	US-09-252-991A-30963	Sequence 30963, A
249	20	87.0	199	3	US-08-737-248-7	Sequence 7, Appli	322	20	87.0	280	4	US-09-660-587-11	Sequence 11, Appli
250	20	87.0	199	3	US-08-737-248-8	Sequence 8, Appli	323	20	87.0	280	4	US-09-261-358A-11	Sequence 11, Appli
251	20	87.0	199	3	US-08-737-248-9	Sequence 9, Appli	324	20	87.0	280	4	US-09-201-458-7	Sequence 7, Appli
252	20	87.0	199	3	US-08-737-248-10	Sequence 10, Appli	325	20	87.0	280	4	US-09-314-701-6	Sequence 6, Appli
253	20	87.0	199	3	US-08-737-248-12	Sequence 12, Appli	326	20	87.0	280	4	US-09-811-007A-11	Sequence 11, Appli
254	20	87.0	199	3	US-08-737-248-14	Sequence 14, Appli	327	20	87.0	280	4	US-09-252-991A-24898	Sequence 24898, A
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256	20	87.0	205	4	US-09-134-000C-4719	Sequence 4719, Ap	329	20	87.0	287	4	US-09-660-587-8	Sequence 8, Appli
257	20	87.0	207	4	US-09-252-991A-23680	Sequence 23680, A	330	20	87.0	287	4	US-09-261-358A-8	Sequence 8, Appli
258	20	87.0	208	4	US-09-252-991A-27061	Sequence 27061, A	331	20	87.0	287	4	US-09-201-458-4	Sequence 4, Appli
259	20	87.0	210	4	US-09-173-300-34	Sequence 34, Appli	332	20	87.0	287	4	US-09-314-701-34	Sequence 34, Appli
260	20	87.0	210	4	US-09-252-991A-28362	Sequence 28362, A	333	20	87.0	287	4	US-09-252-991A-30447	Sequence 30447, A
261	20	87.0	211	4	US-09-205-258-263	Sequence 263, App	334	20	87.0	287	4	US-09-553-662-19	Sequence 19, Appli
262	20	87.0	217	4	US-09-252-991A-19563	Sequence 19563, A	335	20	87.0	287	4	US-09-553-662-19	Sequence 19, Appli
263	20	87.0	219	4	US-09-252-991A-18278	Sequence 18278, A	336	20	87.0	287	4	US-10-062-994-19	Sequence 8, Appli
264	20	87.0	221	1	US-07-903-710-6	Sequence 6, Appli	337	20	87.0	287	4	US-09-811-007A-8	Sequence 8, Appli
265	20	87.0	221	1	US-08-252-966B-8	Sequence 8, Appli	338	20	87.0	288	4	US-09-252-991A-23449	Sequence 23449, A
266	20	87.0	221	1	US-08-222-638B-6	Sequence 6, Appli	339	20	87.0	292	4	US-09-543-681A-16930	Sequence 5957, Ap
267	20	87.0	221	4	US-09-327-983-14	Sequence 13, Appli	340	20	87.0	292	4	US-09-252-991A-17083	Sequence 17083, A
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270	20	87.0	225	3	US-08-988-251-4	Sequence 4, Appli	343	20	87.0	300	4	US-09-563-997A-48	Sequence 48, Appli
271	20	87.0	225	3	US-08-386-048-4	Sequence 4, Appli	344	20	87.0	303	4	US-09-252-991A-31271	Sequence 31271, A
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276	20	87.0	237	4	US-09-252-991A-23307	Sequence 23307, A	349	20	87.0	308	2	US-08-807-050-3	Sequence 3, Appli
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284	20	87.0	243	2	US-08-836-620A-9	Sequence 9, Appli	357	20	87.0	317	3	US-09-093-522-18	Sequence 18, Appli
285	20	87.0	243	2	US-08-836-620A-10	Sequence 10, Appli	358	20	87.0	317	4	US-09-205-258-504	Sequence 504, App
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	20	87.0	278	4	US-09-811-007A-2	Sequence 2, Appli	393	20	87.0	351	3	US-09-892-188B-2	Sequence 1, Appli

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400	20	87.0	377	2	US-08-853-659A-41	Sequence 41, Appl	473	20	87.0	494	3	US-08-988-251-2	Sequence 2, Appli
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419	20	87.0	406	5	PCT-US91-05801-38	Sequence 38, Appl	492	20	87.0	542	4	US-08-849-180-6	Sequence 6, Appli
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445	20	87.0	452	3	US-09-052-778-15	Sequence 15, Appl	518	20	87.0	606	3	Sequence 3, Appli	Sequence 3, Appli
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454	20	87.0	470	4	US-09-252-991A-29251	Sequence 29251, A	527	20	87.0	614	3	Sequence 10, Appl	Sequence 10, Appl
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543	20	87.0	647	4	US-09-252-991A-25652	Sequence 25652, A	616	20	87.0	890	5	PCT-US94-00545-5	Sequence 5, Appli
544	20	87.0	651	3	US-08-693-940-3	Sequence 3, Appli	617	20	87.0	892	4	PCT-US94-00545-5	Sequence 16, Appli
545	20	87.0	651	4	US-09-566-660-3	Sequence 3, Appli	618	20	87.0	894	2	US-09-585-858-16	Sequence 16, Appli
546	20	87.0	651	4	US-09-252-991A-28603	Sequence 28603, A	619	20	87.0	896	4	US-08-867-941-15	Sequence 15, Appli
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548	20	87.0	654	4	US-09-252-991A-25423	Sequence 25423, A	621	20	87.0	901	4	US-08-867-941-11	Sequence 11, Appli
549	20	87.0	655	1	US-07-736-178C-2	Sequence 2, Appli	622	20	87.0	912	4	US-09-252-991A-25653	Sequence 25653, A
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553	20	87.0	673	4	US-09-252-991A-29219	Sequence 29219, A	626	20	87.0	919	4	US-09-489-039A-10199	Sequence 10199, A
554	20	87.0	687	4	US-09-252-991A-31650	Sequence 31650, A	627	20	87.0	921	1	US-08-396-479B-2	Sequence 2, Appli
555	20	87.0	687	4	US-09-328-352-5840	Sequence 5840, Ap	628	20	87.0	921	1	US-08-818-823-2	Sequence 2, Appli
556	20	87.0	691	4	US-09-252-991A-31413	Sequence 31413, A	629	20	87.0	921	1	US-08-818-823-2	Sequence 2, Appli
557	20	87.0	692	4	US-09-540-236-2750	Sequence 2750, Ap	630	20	87.0	921	1	US-08-818-823-2	Sequence 2, Appli
558	20	87.0	695	1	US-07-671-817A-5	Sequence 5, Appli	631	20	87.0	921	1	US-08-818-823-2	Sequence 2, Appli
559	20	87.0	699	5	PCT-US94-07297-39	Sequence 39, Appli	632	20	87.0	921	1	US-08-818-823-2	Sequence 2, Appli
560	20	87.0	704	4	US-09-252-991A-20734	Sequence 20734, A	633	20	87.0	923	4	US-09-252-991A-22509	Sequence 22509, A
561	20	87.0	707	4	US-09-252-991A-18542	Sequence 18542, A	634	20	87.0	927	4	US-09-134-001C-4831	Sequence 4831, Ap
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564	20	87.0	719	4	US-08-765-907A-15	Sequence 15, Appli	637	20	87.0	940	4	US-09-540-236-2645	Sequence 2645, Ap
565	20	87.0	722	4	US-09-252-991A-22811	Sequence 22811, A	638	20	87.0	940	4	US-09-252-991A-17014	Sequence 17014, A
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567	20	87.0	724	1	US-08-835-268-62	Sequence 62, Appli	640	20	87.0	976	4	US-07-671-817A-6	Sequence 6, Appli
568	20	87.0	724	2	US-09-060-692-62	Sequence 62, Appli	641	20	87.0	1008	4	US-09-252-991A-30838	Sequence 30838, A
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571	20	87.0	724	5	PCT-US94-10151A-62	Sequence 62, Appli	644	20	87.0	1049	4	US-09-107-532A-5966	Sequence 5966, Ap
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573	20	87.0	731	4	US-09-252-991A-17180	Sequence 17180, A	646	20	87.0	1052	3	US-08-863-118-1	Sequence 2, Appli
574	20	87.0	733	3	US-09-073-587-3	Sequence 3, Appli	647	20	87.0	1052	3	US-08-863-118-1	Sequence 2, Appli
575	20	87.0	734	4	US-09-442-055-2	Sequence 4, Appli	648	20	87.0	1052	3	US-08-863-118-1	Sequence 2, Appli
576	20	87.0	734	4	US-09-442-055-2	Sequence 4, Appli	649	20	87.0	1052	3	US-08-863-118-1	Sequence 2, Appli
577	20	87.0	735	4	US-09-252-991A-17053	Sequence 17053, A	650	20	87.0	1052	3	US-08-863-118-1	Sequence 2, Appli
578	20	87.0	738	4	US-09-252-991A-27291	Sequence 27291, A	651	20	87.0	1052	3	US-08-863-118-1	Sequence 2, Appli
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584	20	87.0	762	4	US-09-252-991A-28078	Sequence 28078, A	657	20	87.0	1142	3	US-08-304-871-12	Sequence 12, Appli
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586	20	87.0	765	2	US-08-663-112-2	Sequence 2, Appli	659	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
587	20	87.0	773	3	US-08-564-264-1	Sequence 1, Appli	660	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
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591	20	87.0	792	4	US-09-252-991A-25776	Sequence 25776, A	664	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
592	20	87.0	796	4	US-09-252-991A-17490	Sequence 17490, A	665	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
593	20	87.0	801	4	US-09-252-991A-27870	Sequence 27870, A	666	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
594	20	87.0	803	4	US-09-252-991A-30479	Sequence 30479, A	667	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
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597	20	87.0	826	4	US-09-894-998A-47	Sequence 47, Appli	670	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
598	20	87.0	833	3	US-08-699-103B-4	Sequence 4, Appli	671	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
599	20	87.0	833	4	US-09-229-059-4	Sequence 4, Appli	672	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
600	20	87.0	833	4	US-08-628-133-4	Sequence 4, Appli	673	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
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603	20	87.0	845	4	US-09-252-991A-17856	Sequence 17856, A	676	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
604	20	87.0	851	4	US-09-252-991A-22021	Sequence 22021, A	677	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
605	20	87.0	852	4	US-09-585-858-19	Sequence 19, Appli	678	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
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607	20	87.0	856	4	US-09-252-991A-25593	Sequence 25593, A	680	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
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610	20	87.0	869	4	US-09-489-039A-11429	Sequence 11429, A	683	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli
611	20	87.0	871	3	US-09-245-041-19	Sequence 19, Appli	684	20	87.0	1151	1	US-08-349-867-19	Sequence 19, Appli

685	20	87.0	1177	3	US-08-922-505A-14	Sequence 14, Appl	758	20	87.0	1181	4	US-09-547-422-11	Sequence 11, Appl
686	20	87.0	1177	3	US-08-922-505A-26	Sequence 26, Appl	759	20	87.0	1181	4	US-09-547-422-13	Sequence 13, Appl
687	20	87.0	1177	3	US-08-922-505A-28	Sequence 28, Appl	760	20	87.0	1181	4	US-09-547-422-15	Sequence 15, Appl
688	20	87.0	1177	3	US-08-922-505A-34	Sequence 34, Appl	761	20	87.0	1181	4	US-09-547-422-17	Sequence 17, Appl
689	20	87.0	1177	3	US-09-260-952A-10	Sequence 10, Appl	762	20	87.0	1181	4	US-09-547-422-28	Sequence 28, Appl
690	20	87.0	1177	3	US-09-260-952A-12	Sequence 12, Appl	763	20	87.0	1181	4	US-09-417-197-133	Sequence 133, Appl
691	20	87.0	1177	3	US-09-260-952A-14	Sequence 14, Appl	764	20	87.0	1182	1	US-08-349-867-34	Sequence 34, Appl
692	20	87.0	1177	3	US-09-260-952A-26	Sequence 26, Appl	765	20	87.0	1182	2	US-08-598-305A-34	Sequence 34, Appl
693	20	87.0	1177	3	US-09-260-952A-28	Sequence 28, Appl	766	20	87.0	1188	1	US-08-233-476-34	Sequence 34, Appl
694	20	87.0	1177	3	US-09-253-341-10	Sequence 10, Appl	767	20	87.0	1188	5	US-08-639-923A-34	Sequence 34, Appl
695	20	87.0	1177	3	US-09-253-341-12	Sequence 12, Appl	768	20	87.0	1188	8	US-08-602-737-8	Sequence 8, Appl
696	20	87.0	1177	3	US-09-253-341-26	Sequence 26, Appl	769	20	87.0	1193	3	US-08-754-490-30	Sequence 30, Appl
697	20	87.0	1177	3	US-09-253-341-34	Sequence 34, Appl	770	20	87.0	1193	3	US-08-922-505A-30	Sequence 30, Appl
698	20	87.0	1177	3	US-09-253-331A-10	Sequence 10, Appl	771	20	87.0	1193	3	US-09-001-982-8	Sequence 8, Appl
699	20	87.0	1177	3	US-09-253-331A-12	Sequence 12, Appl	772	20	87.0	1193	3	US-09-260-952A-30	Sequence 30, Appl
700	20	87.0	1177	3	US-09-253-331A-26	Sequence 26, Appl	773	20	87.0	1193	3	US-09-253-341-30	Sequence 30, Appl
701	20	87.0	1177	3	US-09-253-331A-34	Sequence 34, Appl	774	20	87.0	1193	3	US-09-253-331A-30	Sequence 30, Appl
702	20	87.0	1177	3	US-09-261-040-10	Sequence 10, Appl	775	20	87.0	1193	3	US-09-261-040-30	Sequence 30, Appl
703	20	87.0	1177	3	US-09-261-040-12	Sequence 12, Appl	776	20	87.0	1193	3	US-09-261-040-30	Sequence 30, Appl
704	20	87.0	1177	3	US-09-261-040-14	Sequence 14, Appl	777	20	87.0	1193	3	US-09-916-956A-30	Sequence 30, Appl
705	20	87.0	1177	3	US-09-261-040-26	Sequence 26, Appl	778	20	87.0	1193	3	US-09-873-873-30	Sequence 30, Appl
706	20	87.0	1177	3	US-09-261-040-34	Sequence 34, Appl	779	20	87.0	1193	3	US-09-997-914-30	Sequence 30, Appl
707	20	87.0	1177	3	US-09-261-040-10	Sequence 10, Appl	780	20	87.0	1194	2	US-08-680-326-35	Sequence 35, Appl
708	20	87.0	1177	3	US-09-261-040-12	Sequence 12, Appl	781	20	87.0	1198	3	US-09-794-236-3	Sequence 131, Appl
709	20	87.0	1177	3	US-09-261-040-26	Sequence 26, Appl	782	20	87.0	1217	4	US-09-252-991A-26104	Sequence 26104, A
710	20	87.0	1177	3	US-09-261-040-34	Sequence 34, Appl	783	20	87.0	1235	4	US-08-680-326-36	Sequence 36, Appl
711	20	87.0	1177	3	US-09-916-956A-10	Sequence 10, Appl	784	20	87.0	1235	4	US-09-904-065-6	Sequence 6, Appl
712	20	87.0	1177	3	US-09-916-956A-12	Sequence 12, Appl	785	20	87.0	1235	4	US-09-904-065-8	Sequence 8, Appl
713	20	87.0	1177	3	US-09-916-956A-14	Sequence 14, Appl	786	20	87.0	1235	4	US-09-904-065-10	Sequence 10, Appl
714	20	87.0	1177	3	US-09-916-956A-26	Sequence 26, Appl	787	20	87.0	1235	4	US-09-904-065-16	Sequence 16, Appl
715	20	87.0	1177	3	US-09-916-956A-34	Sequence 34, Appl	788	20	87.0	1235	4	US-09-904-065-17	Sequence 17, Appl
716	20	87.0	1177	3	US-09-873-873-10	Sequence 10, Appl	789	20	87.0	1235	4	US-09-904-065-18	Sequence 18, Appl
717	20	87.0	1177	3	US-09-873-873-12	Sequence 12, Appl	790	20	87.0	1235	4	US-09-904-065-19	Sequence 19, Appl
718	20	87.0	1177	3	US-09-873-873-14	Sequence 14, Appl	791	20	87.0	1238	4	US-09-252-991A-26363	Sequence 26363, A
719	20	87.0	1177	3	US-09-873-873-16	Sequence 16, Appl	792	20	87.0	1238	4	US-09-904-065-2	Sequence 2, Appl
720	20	87.0	1177	3	US-09-873-873-28	Sequence 28, Appl	793	20	87.0	1238	4	US-09-904-065-14	Sequence 14, Appl
721	20	87.0	1177	3	US-09-997-914-10	Sequence 10, Appl	794	20	87.0	1240	4	US-08-680-326-37	Sequence 37, Appl
722	20	87.0	1177	3	US-09-997-914-12	Sequence 12, Appl	795	20	87.0	1240	4	US-09-904-065-4	Sequence 4, Appl
723	20	87.0	1177	3	US-09-997-914-14	Sequence 14, Appl	796	20	87.0	1240	4	US-09-904-065-15	Sequence 15, Appl
724	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	797	20	87.0	1260	3	US-09-245-041-2	Sequence 2, Appl
725	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	798	20	87.0	1318	4	US-09-540-236-3623	Sequence 3623, Ap
726	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	799	20	87.0	1350	4	US-09-245-041-17	Sequence 17, Appl
727	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	800	20	87.0	1350	4	US-09-252-991A-17932	Sequence 17932, A
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729	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	802	20	87.0	1427	4	US-09-252-991A-20577	Sequence 20577, A
730	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	803	20	87.0	1427	4	US-09-252-991A-27005	Sequence 27005, A
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732	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	805	20	87.0	1523	4	US-09-182-024A-2	Sequence 2, Appl
733	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	806	20	87.0	1554	4	US-09-252-991A-26814	Sequence 26814, A
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735	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	808	20	87.0	1554	4	US-09-962-284-2	Sequence 2, Appl
736	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	809	20	87.0	1554	4	US-09-845-583A-6	Sequence 6, Appl
737	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	810	20	87.0	1554	4	US-09-074-658-15	Sequence 15, Appl
738	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	811	20	87.0	1554	4	US-09-074-658-11	Sequence 11, Appl
739	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	812	20	87.0	1554	4	US-09-252-991A-17052	Sequence 17052, A
740	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	813	20	87.0	1554	4	US-09-245-041-15	Sequence 15, Appl
741	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	814	20	87.0	1554	4	US-08-460-309-5	Sequence 5, Appl
742	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	815	20	87.0	1554	4	US-08-125-077-5	Sequence 5, Appl
743	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	816	20	87.0	1554	4	US-09-036-987A-4	Sequence 4, Appl
744	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	817	20	87.0	1554	4	US-09-370-700-4	Sequence 4, Appl
745	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	818	20	87.0	1554	4	US-09-428-517-3	Sequence 3, Appl
746	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	819	20	87.0	1554	4	US-08-714-741-32	Sequence 32, Appl
747	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	820	20	87.0	1554	4	US-08-041-774-1	Sequence 1, Appl
748	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	821	20	87.0	1554	4	US-08-530-340-7	Sequence 7, Appl
749	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	822	20	87.0	1554	4	US-08-939-002A-8	Sequence 8, Appl
750	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	823	20	87.0	1554	4	US-08-469-141A-9	Sequence 9, Appl
751	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	824	20	87.0	1554	4	US-08-469-141A-26	Sequence 26, Appl
752	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	825	20	87.0	1554	4	US-08-469-141A-26	Sequence 26, Appl
753	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	826	20	87.0	1554	4	US-08-469-141A-26	Sequence 26, Appl
754	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	827	20	87.0	1554	4	US-08-469-141A-26	Sequence 26, Appl
755	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	828	20	87.0	1554	4	US-08-469-141A-26	Sequence 26, Appl
756	20	87.0	1177	3	US-09-997-914-26	Sequence 26, Appl	829	20	87.0	1554	4	US-08-469-141A-26	Sequence 26, Appl
757	20	87.0	1177	3	US-09-997-914-34	Sequence 34, Appl	830	20	87.0	1554	4	US-08-469-141A-26	Sequence 26, Appl

831	19	82.6	22	4	US-09-120-653D-13	Sequence 13, Appl	904	19	82.6	155	4	US-09-732-210-1636	Sequence 1636, Ap
832	19	82.6	35	2	US-08-142-551B-115	Sequence 115, App	905	19	82.6	155	4	US-09-732-210-1637	Sequence 1637, Ap
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## ALIGNMENTS

RESULT 1  
US-09-165-926-1  
; Sequence 1, Application US/09165926  
; Patent No. 6461875  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Or, David  
; APPLICANT: Lau, Edward  
; APPLICANT: Winkler, James V.  
; TITLE OF INVENTION: Test for Rapid Evaluation of Ischemic States and Kit  
; FILE REFERENCE: ISC35269-183796  
; CURRENT APPLICATION NUMBER: US/09/165,926  
; CURRENT FILING DATE: 1998-10-02  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-165-926-1

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Db 1 DAHK 4

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; Sequence 1, Application US/09165961  
; Patent No. 6475743  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Or, David  
; APPLICANT: Lau, Edward  
; TITLE OF INVENTION: MARKER USEFUL FOR DETECTION AND MEASUREMENT OF FREE  
; TITLE OF INVENTION: RADICAL DAMAGE AND METHOD  
; FILE REFERENCE: 4172-15  
; CURRENT APPLICATION NUMBER: US/09/165,961  
; CURRENT FILING DATE: 1998-10-02  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1

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US-09-165-961-1

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; Patent No. 6492179  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Or, David  
; APPLICANT: Lau, Edward  
; APPLICANT: Winkler, James V.  
; TITLE OF INVENTION: Test for Rapid Evaluation of Ischemic States and Kit  
; FILE REFERENCE: ISC35269-183797  
; CURRENT APPLICATION NUMBER: US/09/165,581  
; CURRENT FILING DATE: 1998-10-02  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
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; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-165-581-1

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; Patent No. 5650307  
; GENERAL INFORMATION:  
; APPLICANT: Sijmons, Peter C.  
; APPLICANT: Hoekema, Andreas  
; APPLICANT: Dekker, Bernardus M.M.  
; APPLICANT: Schrammeijer, Barbara  
; APPLICANT: Verwoerd, Tewis C.  
; APPLICANT: VandenElzen, Petrus J.M.  
; TITLE OF INVENTION: PRODUCTION OF HETEROLOGOUS PROTEINS IN  
; TITLE OF INVENTION: PLANTS AND PLANT CELLS  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 Pennsylvania Avenue, NW, Ste. 5500  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812  
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; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/469,856  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 800

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; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 6192-0025.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)887-1500
; TELEFAX: (202)887-0763
; TELEX: 90-4030 MRSNFOERSWSH
; INFORMATION FOR SEQ ID NO: 10:
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; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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US-08-469-856-10

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DB      1 DAHK 4

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; Patent No. 6461875
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Lau, Edward
; APPLICANT: Winkler, James V.
; TITLE OF INVENTION: Test for Rapid Evaluation of Ischemic States and Kit
; FILE REFERENCE: ISC35269-183796
; CURRENT APPLICATION NUMBER: US/09/165,926
; CURRENT FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
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US-09-165-926-2

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DB      1 DAHK 4

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; Patent No. 6475743
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Lau, Edward
; TITLE OF INVENTION: MARKER USEFUL FOR DETECTION AND MEASUREMENT OF FREE
; FILE REFERENCE: 4172-15
; CURRENT APPLICATION NUMBER: US/09/165,961
; CURRENT FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.1
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US-09-165-961-2
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DB      1 DAHK 4

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; Patent No. 6492179
; GENERAL INFORMATION:
; APPLICANT: Bar-Or, David
; APPLICANT: Lau, Edward
; APPLICANT: Winkler, James V.
; TITLE OF INVENTION: Test for Rapid Evaluation of Ischemic States and Kit
; FILE REFERENCE: ISC35269-183797
; CURRENT APPLICATION NUMBER: US/09/165,581
; CURRENT FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
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US-09-165-581-2

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DB      1 DAHK 4

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; Patent No. 5650307
; GENERAL INFORMATION:
; APPLICANT: Sijmons, Peter C.
; APPLICANT: Hoekema, Andreas
; APPLICANT: Dekker, Bernardus M.M.
; APPLICANT: Schrammeijer, Barbara
; APPLICANT: Verwoerd, Tewniss C.
; APPLICANT: VandenElzen, Petrus J.M.
; TITLE OF INVENTION: PRODUCTION OF HETEROLOGOUS PROTEINS IN
; TITLE OF INVENTION: PLANTS AND PLANT CELLS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 Pennsylvania Avenue, NW, Ste. 5500
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1812
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,856
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 6192-0025.01
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TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)887-1500  
TELEFAX: (202)887-0763  
TELEX: 90-4030 MESNFOERSWSH  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-469-856-9

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## RESULT 9

US-08-702-572-13  
Sequence 13, Application US/08702572  
Patent No. 5965386

GENERAL INFORMATION:  
APPLICANT: Kerry-Williams, Sean M  
APPLICANT: Gilbert, Sarah C  
TITLE OF INVENTION: Yeast Strains and Modified Albumins  
NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Centeon L.L.C.  
STREET: 1020 First Avenue  
CITY: King of Prussia  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 19406-1310

COMPUTER READABLE FORM:  
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COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/702,572  
FILING DATE: 11-NOV-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: WO 95/23857  
FILING DATE: 1-MAR-1995  
APPLICATION NUMBER: GB 9404270.2  
FILING DATE: 5-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Naomi Biswas  
REGISTRATION NUMBER: 39,384  
REFERENCE/DOCKET NUMBER: CE0114 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610/878/4294  
TELEFAX: 610/878/4221

INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-702-572-13

Query Match 100.0%; Score 23; DB 2; Length 24;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
|  
|  
|  
|  
Db 20 DAHK 23

## RESULT 10

US-09-846-329A-1  
Sequence 1, Application US/09846329A  
Patent No. 6620786

GENERAL INFORMATION:  
APPLICANT: Jackowski, George  
TITLE OF INVENTION: Biopolymer Marker Indicative of Disease State Having A Molecular Weight of 2937 Daltons  
FILE REFERENCE: 2132.052  
CURRENT APPLICATION NUMBER: US/09/846,329A  
CURRENT FILING DATE: 2001-04-30  
NUMBER OF SEQ ID NOS: 1  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1

LENGTH: 28  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-846-329A-1

Query Match 100.0%; Score 23; DB 4; Length 28;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
|  
|  
|  
|  
Db 2 DAHK 5

## RESULT 11

US-09-480-993-19  
Sequence 19, Application US/09480993  
Patent No. 6383790

GENERAL INFORMATION:  
APPLICANT: Shokat, Kevan M.  
TITLE OF INVENTION: High Affinity Kinase Inhibitors for Target Validation  
FILE REFERENCE: 51538-5001-US  
CURRENT APPLICATION NUMBER: US/09/480,993  
CURRENT FILING DATE: 2000-01-11  
EARLIER APPLICATION NUMBER: US 60/115,340  
EARLIER FILING DATE: 1999-01-11  
NUMBER OF SEQ ID NOS: 20  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 19

LENGTH: 42  
TYPE: PRT  
ORGANISM: Saccharomyces cerevisiae  
FEATURE:  
OTHER INFORMATION: Cdc28, cyclin-dependent kinase  
US-09-480-993-19

Query Match 100.0%; Score 23; DB 4; Length 42;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
|  
|  
|  
|  
Db 15 DAHK 18

## RESULT 12

US-09-134-000C-4709  
Sequence 4709, Application US/09134000C  
Patent No. 6617156

GENERAL INFORMATION:  
APPLICANT: Lynn Doucette-Stamm et al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO



; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778  
; PRIOR FILING DATE: 1997-08-15  
; NUMBER OF SEQ ID NOS: 6812  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4709  
; LENGTH: 68  
; TYPE: PRT  
; ORGANISM: Enterococcus faecalis  
US-09-134-000C-4709

Query Match 100.0%; Score 23; DB 4; Length 68;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
Db 35 DAHK 38

## RESULT 13

US-09-615-192A-316  
; Sequence 316, Application US/09615192A  
; Patent No. 6410718

; GENERAL INFORMATION:  
; APPLICANT: Bloksberg, Leonard N.  
; APPLICANT: Havukkala, Ilkka  
; TITLE OF INVENTION: Materials and Methods for the  
; TITLE OF INVENTION: Modification of Plant Lignin Content  
; FILE REFERENCE: 11000.1003C4U

; CURRENT APPLICATION NUMBER: US/09/615,192A  
; CURRENT FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 08/975,316  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: US 08/713,000  
; PRIOR FILING DATE: 1996-09-11  
; PRIOR APPLICATION NUMBER: US 09/169,789  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 405  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 316  
; LENGTH: 134  
; TYPE: PRT  
; ORGANISM: Pinus radiata  
US-09-615-192A-316

Query Match 100.0%; Score 23; DB 4; Length 134;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
Db 15 DAHK 18

## RESULT 14

US-09-134-001C-4838  
; Sequence 4838, Application US/09134001C  
; Patent No. 6380370

; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14

; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 4838  
; LENGTH: 138  
; TYPE: PRT  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-4838

Query Match 100.0%; Score 23; DB 4; Length 138;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
Db 112 DAHK 115

## RESULT 15

US-09-328-352-7792  
; Sequence 7792, Application US/09328352  
; Patent No. 6562958

; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; CURRENT FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 7792  
; LENGTH: 144  
; TYPE: PRT  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-7792

Query Match 100.0%; Score 23; DB 4; Length 144;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
Db 125 DAHK 128

Search completed: September 9, 2004, 23:48:51  
Job time : 44 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 9, 2004, 23:34:33 ; Search time 113 Seconds

(without alignments)  
11.169 Million cell updates/sec

Title: US-10-076-071-1

Perfect score: 23

Sequence: 1 DAHK 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : SPTREMBL.25.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp Vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_virus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	17	11	Q9QVS7
2	23	100.0	21	11	Q9QVA1
3	23	100.0	47	13	Q91093
4	23	100.0	50	17	Q82228
5	23	100.0	56	16	Q88VE6
6	23	100.0	59	10	Q42106
7	23	100.0	66	13	Q91889
8	23	100.0	73	9	Q852W2
9	23	100.0	81	11	Q9R0N2
10	23	100.0	82	9	Q8W6D6
11	23	100.0	82	12	Q56843
12	23	100.0	83	9	Q852V3
13	23	100.0	84	2	Q9RG01
14	23	100.0	87	16	Q9JUN5
15	23	100.0	88	16	Q7VBB7
16	23	100.0	90	17	Q8PYS4

17	23	100.0	91	11	Q9CW67
18	23	100.0	92	2	Q9ZBL9
19	23	100.0	94	16	Q8PG46
20	23	100.0	94	16	Q8ZCA4
21	23	100.0	95	16	Q8R853
22	23	100.0	95	16	Q89RT9
23	23	100.0	96	11	Q8R444
24	23	100.0	99	12	Q9PVV5
25	23	100.0	100	16	Q9CFM0
26	23	100.0	102	16	Q9RFX8
27	23	100.0	104	2	Q9RG04
28	23	100.0	104	2	Q9RFZ8
29	23	100.0	104	16	Q8XY22
30	23	100.0	107	2	Q93DW4
31	23	100.0	109	1	Q59658
32	23	100.0	109	17	Q8T1J7
33	23	100.0	110	4	Q9BX06
34	23	100.0	110	5	Q86FH2
35	23	100.0	110	16	Q7V709
36	23	100.0	112	16	Q8U5H1
37	23	100.0	114	2	Q9RG07
38	23	100.0	116	2	Q9RAI9
39	23	100.0	116	2	Q9RPP5
40	23	100.0	116	10	Q7XS09
41	23	100.0	118	5	Q9VTJ8
42	23	100.0	118	17	Q980X5
43	23	100.0	120	5	Q8IJ28
44	23	100.0	120	11	Q9D629
45	23	100.0	121	16	Q88061
46	23	100.0	122	16	Q9RTW6
47	23	100.0	122	16	P71946
48	23	100.0	124	10	Q65828
49	23	100.0	125	16	Q9TRJ0
50	23	100.0	128	10	Q8W1R0
51	23	100.0	128	16	Q7U5Y0
52	23	100.0	131	3	Q9U066
53	23	100.0	132	5	Q95XK0
54	23	100.0	132	12	Q9DST6
55	23	100.0	136	3	Q60092
56	23	100.0	137	11	Q8R213
57	23	100.0	139	16	Q890L9
58	23	100.0	143	10	Q8GUU1
59	23	100.0	144	8	Q952U2
60	23	100.0	146	16	Q88ZNE
61	23	100.0	148	2	Q9S4L7
62	23	100.0	151	16	Q8CJQ5
63	23	100.0	154	16	Q8DDH2
64	23	100.0	155	16	Q9PGZ2
65	23	100.0	155	16	Q8NPV6
66	23	100.0	156	10	Q948A5
67	23	100.0	156	10	Q7XFK9
68	23	100.0	157	10	Q84X70
69	23	100.0	162	16	Q9ED40
70	23	100.0	165	4	Q8TA18
71	23	100.0	166	2	Q9S4Z3
72	23	100.0	168	2	Q87496
73	23	100.0	168	2	Q84GY4
74	23	100.0	168	2	Q8XGT6
75	23	100.0	169	16	Q8XHQ9
76	23	100.0	171	5	Q9VH17
77	23	100.0	171	11	Q9ERG9
78	23	100.0	172	16	Q87F15
79	23	100.0	173	2	Q9S422
80	23	100.0	173	16	Q7WNR3
81	23	100.0	173	16	Q7WB95
82	23	100.0	173	16	Q7VVG1
83	23	100.0	174	13	Q8AXT6
84	23	100.0	175	2	Q53910
85	23	100.0	175	10	Q40848
86	23	100.0	176	16	Q9L001
87	23	100.0	177	16	Q8NMG3
88	23	100.0	179	16	Q8YBD1
89	23	100.0	179	16	Q8FX12

Q9CW67 mus musculus  
Q9ZBL9 mycobacteri  
Q8PG46 xanthomonas  
Q8ZCA4 versinia pe  
Q8R853 thermoanaer  
Q89RT9 bradyrhizob  
Q8444 phodopus su  
Q9PVV5 xestia c-ni  
Q9CFM0 lactococcus  
Q9RFX8 deinococcus  
Q9RG04 mycoplasma  
Q9RFZ8 mycoplasma  
Q8XY22 ralstonia s  
Q93DW4 mycoplasma  
Q59658 methanosarc  
Q8T1J7 methanosarc  
Q9BX06 homo sapien  
Q86FH2 schistosoma  
Q7V709 prochloroco  
Q8U5H1 agrobacteri  
Q9RG07 mycoplasma  
Q9RAI9 mycoplasma  
Q9RPP5 ehrlichia c  
Q9XS09 oryza sativ  
Q9VTJ8 drosophila  
Q980X5 sulfolobus  
Q8IJ28 plasmodium  
Q9D629 mus musculus  
Q88061 streptomyce  
Q9RTW6 deinococcus  
P71946 mycobacteri  
Q65828 lycopersico  
Q9TRJ0 neisseria m  
Q8W1R0 cynodon dac  
Q7U5Y0 synecococc  
Q9U066 schizosacch  
Q95XK0 caenorhabdi  
Q9DST6 ascovirus d  
Q60092 schizosacch  
Q8R213 mus musculus  
Q890L9 clostridium  
Q8GUU1 arabidopsis  
Q952U2 stigmatopor  
Q88ZNE lactobacill  
Q9S4L7 staphylococ  
Q9CJQ5 pasteurella  
Q8DDH2 vibrio vuln  
Q9PGZ2 xyella fas  
Q8NPV6 corynebacte  
Q948A5 oryza sativ  
Q7XFK9 oryza sativ  
Q84X70 chlamydomon  
Q9ED40 rhizobium l  
Q8TA18 homo sapien  
Q9S4Z3 ehrlichia m  
Q87496 versinia en  
Q84GY4 photorhabdu  
Q84GT6 versinia en  
Q8XHQ9 clostridium  
Q9VH17 drosophila  
Q9ERG9 mesocricetu  
Q87F15 xyella fas  
Q9S422 ehrlichia m  
Q7WNR3 bordetella  
Q7WB95 bordetella  
Q7VVG1 bordetella  
Q8AXT6 sparus aura  
Q53910 streptomyce  
Q40848 picea glauc  
Q9L001 streptomyce  
Q8NMG3 corynebacte  
Q8YBD1 bruceella me  
Q8FX12 bruceella su

90	23	100.0	179	16	Q83LW5	Q83LW5 shigella fl	163	23	100.0	273	16	Q8CTH3	Q8cth3 staphylococ
91	23	100.0	184	16	Q83I08	Q83i08 tropheryma	164	23	100.0	274	16	Q8EAX3	Q8eax3 shewanella
92	23	100.0	184	16	Q83G62	Q83g62 tropheryma	165	23	100.0	275	16	Q8CW09	Q8cw09 escherichia
93	23	100.0	185	16	Q8DEA7	Q8dea7 vibrio vuln	166	23	100.0	276	16	Q7UAI1	Q7uail shigella fl
94	23	100.0	185	16	Q8DBE6	Q8dbe6 vibrio vuln	167	23	100.0	276	2	Q9F475	Q9f475 ehrlichia c
95	23	100.0	187	16	Q99TA5	Q99ta5 staphylococ	168	23	100.0	276	2	Q9KUJ1	Q9kju1 peanut witec
96	23	100.0	187	16	Q8EIX9	Q8eix9 shewanella	169	23	100.0	277	2	Q8GGU1	Q8ggul ehrlichia c
97	23	100.0	188	9	Q9ZX37	Q9zx37 bacterioph	170	23	100.0	277	2	Q8G8W7	Q8g8w7 ehrlichia c
98	23	100.0	191	10	Q9C9T5	Q9c9t5 arabidopsis	171	23	100.0	279	2	Q8G8Q1	Q8g8q1 ehrlichia c
99	23	100.0	197	13	Q8JH67	Q8jh67 bufo bufo (	172	23	100.0	280	2	Q52107	Q52107 ehrlichia c
100	23	100.0	198	16	Q83BB7	Q83bb7 enterococcu	173	23	100.0	283	16	Q7WJG1	Q7wjg1 bordetella
101	23	100.0	200	13	Q7SXN7	Q7sxn7 brachydanio	174	23	100.0	283	16	Q7WAC0	Q7wac0 bordetella
102	23	100.0	204	16	Q83XX5	Q83xx5 shigella fl	175	23	100.0	283	16	Q7VZC8	Q7vzc8 bordetella
103	23	100.0	206	16	Q8PK43	Q8pk43 xanthomonas	176	23	100.0	284	16	Q7W3C5	Q7w3c5 bordetella
104	23	100.0	209	16	Q9RZ87	Q9rzt87 deinococcus	177	23	100.0	285	16	Q8U9L1	Q8u9l1 agrobacteri
105	23	100.0	210	11	Q8BKL0	Q8bkl0 mus musculu	178	23	100.0	285	17	Q58608	Q58608 pyrococcus
106	23	100.0	211	5	Q21501	Q21501 caenorhabdi	179	23	100.0	286	16	Q9PPY5	Q9ppy5 ureaplasma
107	23	100.0	211	10	Q9SHT7	Q9sht7 arabidopsis	180	23	100.0	286	16	Q7WEP4	Q7wep4 bordetella
108	23	100.0	212	4	Q15188	Q15188 homo sapien	181	23	100.0	287	9	Q8LTQ8	Q8ltq8 lactococcus
109	23	100.0	212	16	Q915B3	Q915b3 pseudomonas	182	23	100.0	287	16	Q7VU32	Q7vu32 bordetella
110	23	100.0	213	15	Q91027	Q91027 human immu	183	23	100.0	288	2	Q9ZGJ2	Q9zgj2 ehrlichia c
111	23	100.0	216	5	Q8T010	Q8t010 drosophila	184	23	100.0	288	5	Q8WPU9	Q8wpv9 suberites d
112	23	100.0	216	13	Q9DET0	Q9det0 dicentrarch	185	23	100.0	288	10	Q9XHZ7	Q9xhz7 arabidopsis
113	23	100.0	219	16	Q8DFX3	Q8dpf3 streptococc	186	23	100.0	289	4	Q9H9M2	Q9h9m2 homo sapien
114	23	100.0	219	17	Q8U4N0	Q8u4n0 pyrococcus	187	23	100.0	289	4	Q8TB37	Q8tb37 homo sapien
115	23	100.0	220	11	Q8CA60	Q8ca60 mus musculu	188	23	100.0	289	12	Q7T658	Q7t658 human rhino
116	23	100.0	220	16	Q8CUB5	Q8cub5 staphylococ	189	23	100.0	289	16	Q8ZHH5	Q8zhh5 yersinia pe
117	23	100.0	222	5	Q9NF94	Q9nf94 leishmania	190	23	100.0	290	5	Q19684	Q19684 caenorhabdi
118	23	100.0	222	16	Q8DVJ4	Q8dvj4 streptococc	191	23	100.0	290	16	Q889R3	Q889r3 pseudomonas
119	23	100.0	224	5	Q9NAD4	Q9nad4 caenorhabdi	192	23	100.0	295	16	Q9CPA0	Q9cpa0 pasteurella
120	23	100.0	225	2	Q8RL80	Q8rl80 mycoplasma	193	23	100.0	298	2	P74836	P74836 sphingomona
121	23	100.0	226	16	Q910E4	Q910e4 pseudomonas	194	23	100.0	298	13	Q7ZVA2	Q7zva2 brachydanio
122	23	100.0	229	2	Q93EB3	Q93eb3 rhizobium l	195	23	100.0	299	16	Q97IK1	Q97ik1 clostridium
123	23	100.0	229	16	Q930J3	Q930j3 rhizobium m	196	23	100.0	300	12	Q919R6	Q919r6 white spot
124	23	100.0	229	16	Q8UBV8	Q8ubv8 agrobacteri	197	23	100.0	302	12	Q91LC5	Q91lc5 white spot
125	23	100.0	230	6	Q8QS56	Q8qs56 sus scrofa	198	23	100.0	302	12	Q7T9Q2	Q7t9q2 adoxophyes
126	23	100.0	230	9	Q64121	Q64121 bacterioph	199	23	100.0	304	16	Q87Q15	Q87q15 vibrio para
127	23	100.0	231	16	Q34581	Q34581 bacillus su	200	23	100.0	305	16	Q8CZS8	Q8czs8 yersinia pe
128	23	100.0	231	2	Q93M48	Q93m48 bacillus th	201	23	100.0	306	10	Q943K3	Q943k3 oryza sativ
129	23	100.0	231	13	Q8AWF0	Q8awf0 epinephelus	202	23	100.0	307	5	Q9VJ94	Q9vj94 drosophila
130	23	100.0	231	13	Q8AVAI	Q8aai epinephelus	203	23	100.0	312	16	Q98K09	Q98k09 rhizobium l
131	23	100.0	231	13	Q7TIA9	Q7tia9 perca flave	204	23	100.0	312	16	Q88DM6	Q88dm6 pseudomonas
132	23	100.0	232	10	Q9LVV7	Q9lvv7 arabidopsis	205	23	100.0	313	5	Q7YZX5	Q7yzx5 trypanosoma
133	23	100.0	235	16	Q9KTT4	Q9ktg4 vibrio chol	206	23	100.0	313	16	Q8F7M9	Q8f7m9 leptospira
134	23	100.0	235	16	Q8EPA6	Q8epa6 oceanobacil	207	23	100.0	314	2	Q8GIY6	Q8giy6 mycoplasma
135	23	100.0	236	17	Q8UOL7	Q8uol7 pyrococcus	208	23	100.0	315	16	Q7WQ23	Q7wq23 bordetella
136	23	100.0	244	5	Q9V5C8	Q9v5c8 drosophila	209	23	100.0	315	16	Q7WC24	Q7wc24 bordetella
137	23	100.0	245	6	Q95JL3	Q95jl3 pan troglod	210	23	100.0	315	16	Q7VT62	Q7vt62 bordetella
138	23	100.0	246	16	Q83DC4	Q83dc4 coxiella bu	211	23	100.0	316	16	Q92R16	Q92r16 rhizobium m
139	23	100.0	248	12	Q91ID2	Q91id2 lymantria d	212	23	100.0	316	16	Q8DC41	Q8dc41 vibrio vuln
140	23	100.0	248	12	Q99D27	Q99d27 dendrolimus	213	23	100.0	318	4	Q9H8J8	Q9h8j8 homo sapien
141	23	100.0	248	12	Q80HS4	Q80hs4 dendrolimus	214	23	100.0	318	5	Q9BKJ7	Q9bkj7 plasmodium
142	23	100.0	248	12	Q809H2	Q809h2 dendrolimus	215	23	100.0	318	10	Q7YIH6	Q7yih6 oryza sativ
143	23	100.0	248	12	Q8AYI9	Q8ayy9 dendrolimus	216	23	100.0	319	11	Q9CWD8	Q9cwd8 mus musculu
144	23	100.0	249	5	Q9V843	Q9v843 drosophila	217	23	100.0	319	16	Q8YU01	Q8yu01 anabaena sp
145	23	100.0	249	5	Q81308	Q81308 plasmodium	218	23	100.0	320	10	Q8S008	Q8s008 oryza sativ
146	23	100.0	249	10	Q8SLR2	Q8slr2 oryza sativ	219	23	100.0	320	16	Q988Q5	Q988q5 rhizobium l
147	23	100.0	254	11	Q9DA73	Q9da73 mus musculu	220	23	100.0	322	5	Q23796	Q23796 chironomus
148	23	100.0	254	16	Q98KE3	Q98kp3 rhizobium l	221	23	100.0	323	10	Q8L4X3	Q8l4x3 hordeum vul
149	23	100.0	255	2	Q93UZ7	Q93uz7 burkholderi	222	23	100.0	324	16	Q8YAX5	Q8yax5 bruceella me
150	23	100.0	256	16	Q8XHG5	Q8xhg5 clostridium	223	23	100.0	325	10	Q94K10	Q94k10 arabidopsis
151	23	100.0	256	16	Q8X7Z4	Q8x7z4 escherichia	224	23	100.0	326	10	Q9SMG8	Q9smg8 oryza sativ
152	23	100.0	256	16	Q7UDM1	Q7udm1 shigella fl	225	23	100.0	326	10	Q8S7Y2	Q8s7y2 oryza sativ
153	23	100.0	257	16	Q899D8	Q899d8 clostridium	226	23	100.0	326	10	P93675	P93675 oryza sativ
154	23	100.0	258	16	Q8A6J3	Q8a6j3 bacteroides	227	23	100.0	326	10	Q7XHB1	Q7xhb1 oryza sativ
155	23	100.0	259	16	Q83M92	Q83m92 shigella fl	228	23	100.0	328	10	Q8LFR5	Q8lfr5 arabidopsis
156	23	100.0	260	13	Q9W6T2	Q9w6t2 cyprinus ca	229	23	100.0	329	5	Q9VFT0	Q9vft0 drosophila
157	23	100.0	262	16	Q914H1	Q914h1 pseudomonas	230	23	100.0	329	5	Q9Y205	Q9y205 ephydatia f
158	23	100.0	264	12	Q86970	Q86970 equine herp	231	23	100.0	329	10	O04326	O04326 arabidopsis
159	23	100.0	268	2	Q54115	Q54115 saccharopol	232	23	100.0	330	10	O8VYL9	O8vyl9 arabidopsis
160	23	100.0	271	2	Q9KI42	Q9ki42 enterococc	233	23	100.0	330	10	Q9ZRX2	Q9zrx2 triticum ae
161	23	100.0	271	10	Q8S002	Q8s002 oryza sativ	234	23	100.0	330	16	Q97QN8	Q97qn8 streptococ
162	23	100.0	271	16	Q8X284	Q8x284 escherichia	235	23	100.0	330	16	Q8DPQ8	Q8dpq8 streptococ

236	23	100.0	330	16	Q89MF0	Q89mf0 bradyrhizob	309	23	100.0	388	17	Q28907	Q28907 archaeoglob
237	23	100.0	331	2	Q87941	Q87941 thauera aro	310	23	100.0	390	2	Q9X4K9	Q9X4K9 enterococcu
238	23	100.0	331	2	Q92658	Q92658 zymomonas m	311	23	100.0	390	16	Q82UX4	Q82ux4 nitrosomona
239	23	100.0	331	16	Q9CE58	Q9ce58 lactococcus	312	23	100.0	391	16	Q9A486	Q9a486 caulobacter
240	23	100.0	333	3	Q876G5	Q876g5 saccharomyc	313	23	100.0	392	3	Q86Z18	Q86z18 neurospora
241	23	100.0	333	10	Q9ZS77	Q9zs77 hordeum vul	314	23	100.0	392	2	Q47743	Q47743 enterococcu
242	23	100.0	333	16	Q89WC5	Q89wc5 bradyrhizob	315	23	100.0	395	2	Q83U28	Q83u28 enterococcu
243	23	100.0	336	4	Q75794	Q75794 homo sapien	316	23	100.0	396	4	Q81UK7	Q81uk7 homo sapien
244	23	100.0	336	4	Q14107	Q14107 homo sapien	317	23	100.0	396	5	Q81JPA	Q81jp4 plasmodium
245	23	100.0	336	5	Q95RT8	Q95rt8 drosophila	318	23	100.0	396	11	Q8CIF1	Q8cif1 mus musculu
246	23	100.0	336	11	Q62834	Q62834 rattus norv	319	23	100.0	400	12	Q39878	Q39878 hepatitis b
247	23	100.0	336	11	Q8CII12	Q8cii12 mus musculu	320	23	100.0	400	12	Q81125	Q81125 hepatitis b
248	23	100.0	336	11	Q8VE51	Q8ve51 mus musculu	321	23	100.0	400	12	Q39883	Q39883 hepatitis b
249	23	100.0	336	16	Q3KRC1	Q3krc1 vibrio chol	322	23	100.0	400	12	Q9QB56	Q9qb56 hepatitis b
250	23	100.0	337	2	Q9ZH60	Q9zh60 lactobacill	323	23	100.0	400	12	Q81121	Q81121 hepatitis b
251	23	100.0	337	16	Q8CS27	Q8cs27 staphylococ	324	23	100.0	400	12	Q91528	Q91528 hepatitis b
252	23	100.0	337	16	Q8CNT7	Q8cnt7 staphylococ	325	23	100.0	400	12	Q81117	Q81117 hepatitis b
253	23	100.0	337	16	Q8CNT4	Q8cnt4 staphylococ	326	23	100.0	400	12	Q9QB51	Q9qb51 hepatitis b
254	23	100.0	337	16	Q8CM53	Q8cm53 staphylococ	327	23	100.0	400	12	Q9QB50	Q9qb50 hepatitis b
255	23	100.0	337	16	Q8CM53	Q8cm53 staphylococ	328	23	100.0	400	12	Q9QB50	Q9qb50 hepatitis b
256	23	100.0	337	16	Q8CLX8	Q8clx8 staphylococ	329	23	100.0	401	16	Q82Z97	Q82z97 enterococcu
257	23	100.0	339	11	Q921K3	Q921k3 mus musculu	330	23	100.0	403	2	Q9LBQ7	Q9lbq7 enterococcu
258	23	100.0	339	11	Q9DBP1	Q9dbp1 mus musculu	331	23	100.0	403	16	Q8RF12	Q8rf12 fusobacteri
259	23	100.0	340	5	Q9VY87	Q9vy87 drosophila	332	23	100.0	410	2	Q8XK01	Q8xk01 proteus vul
260	23	100.0	340	10	Q3FKG4	Q3fkg4 arabidopsis	333	23	100.0	410	11	Q8BSE0	Q8bse0 mus musculu
261	23	100.0	343	16	Q67849	Q67849 aquifex aeo	334	23	100.0	412	10	Q80485	Q80485 arabidopsis
262	23	100.0	344	5	Q28655	Q28655 sarcophaga	335	23	100.0	412	13	Q12938	Q12938 brachydanio
263	23	100.0	345	5	Q9FG92	Q9fg92 arabidopsis	336	23	100.0	413	4	Q8NCJ3	Q8ncj3 homo sapien
264	23	100.0	345	16	Q88GL3	Q88gl3 pseudomonas	337	23	100.0	413	16	Q88GN7	Q88gn7 pseudomonas
265	23	100.0	346	5	Q81NG9	Q81ng9 drosophila	338	23	100.0	414	4	Q96BC4	Q96bc4 homo sapien
266	23	100.0	347	12	Q84474	Q84474 paramesum	339	23	100.0	414	17	Q27989	Q27989 archaeoglob
267	23	100.0	347	13	Q7SXU9	Q7sxu9 brachydanio	340	23	100.0	415	17	Q8TWD4	Q8twd4 methanopyru
268	23	100.0	347	16	Q99WX3	Q99wx3 staphylococ	341	23	100.0	417	4	Q86VG0	Q86vg0 homo sapien
269	23	100.0	350	5	Q8MZ66	Q8mz66 drosophila	342	23	100.0	419	5	Q95TT9	Q95tt9 drosophila
270	23	100.0	350	16	Q8Y0X3	Q8y0x3 ralstonia s	343	23	100.0	419	16	Q8PJ54	Q8pjs4 xanthomonas
271	23	100.0	350	16	Q8A757	Q8a757 bacteroides	344	23	100.0	419	16	Q8P8C0	Q8p8c0 xanthomonas
272	23	100.0	351	12	Q41046	Q41046 paramesum	345	23	100.0	420	2	Q52501	Q52501 burkholderi
273	23	100.0	352	16	Q82X30	Q82x30 nitrosomona	346	23	100.0	420	9	Q8SDA7	Q8sda7 pseudomonas
274	23	100.0	353	2	Q54816	Q54816 streptomyce	347	23	100.0	420	16	Q89GP9	Q89gp9 bradyrhizob
275	23	100.0	355	13	Q73776	Q73776 gallus gall	348	23	100.0	420	16	Q822D7	Q822d7 chlamydophi
276	23	100.0	356	10	Q93XK9	Q93xk9 lycopersico	349	23	100.0	420	16	Q926P4	Q926p4 chlamydia p
277	23	100.0	356	13	Q7ZUD2	Q7zud2 brachydanio	350	23	100.0	422	16	Q9K1X2	Q9k1x2 chlamydia p
278	23	100.0	358	5	Q9U123	Q9u123 leishmania	351	23	100.0	423	11	Q9D7P9	Q9d7p9 mus musculu
279	23	100.0	358	10	Q04546	Q04546 arabidopsis	352	23	100.0	424	16	Q8P762	Q8p762 xanthomonas
280	23	100.0	359	2	Q93C19	Q93ci9 xanthobacte	353	23	100.0	425	3	Q9P7L2	Q9p7l2 schizosacch
281	23	100.0	361	12	Q72464	Q72464 nelson bay	354	23	100.0	425	4	Q9NQD6	Q9nqd6 homo sapien
282	23	100.0	361	12	Q9DL70	Q9dl70 pseudorabie	355	23	100.0	427	2	Q7WUH3	Q7wuh3 clostridium
283	23	100.0	362	17	Q9YF28	Q9yf28 aeropyrum p	356	23	100.0	427	16	Q9PL61	Q9pl61 chlamydia m
284	23	100.0	364	5	Q9VDM7	Q9vdm7 drosophila	357	23	100.0	430	5	Q44725	Q44725 caenorhabdi
285	23	100.0	364	10	Q8VXE6	Q8vxe6 mesembryant	358	23	100.0	431	5	Q9NCL2	Q9nc12 tribolium c
286	23	100.0	364	10	Q8VXE7	Q8vxe7 mesembryant	359	23	100.0	431	10	Q851V7	Q851v7 oryza sativ
287	23	100.0	364	16	Q07182	Q07182 mycobacteri	360	23	100.0	431	10	Q8LA77	Q8la77 arabidopsis
288	23	100.0	364	16	Q7U191	Q7u191 mycobacteri	361	23	100.0	436	10	Q8GUH8	Q8guh8 arabidopsis
289	23	100.0	365	11	Q9UJJ2	Q9ujj2 mus musculu	362	23	100.0	436	17	Q9HIA6	Q9hia6 thermoplasma
290	23	100.0	365	13	Q91621	Q91621 gallus gall	363	23	100.0	437	5	Q7YVA0	Q7yva0 trypanosoma
291	23	100.0	368	5	Q91845	Q91845 caenorhabdi	364	23	100.0	438	13	Q8AVW9	Q8avw9 xenopus lae
292	23	100.0	368	16	Q8EHC9	Q8ehc9 shewanella	365	23	100.0	440	16	P96718	P96718 bacillus su
293	23	100.0	368	16	Q883W3	Q883w3 pseudomonas	366	23	100.0	440	16	P96718	P96718 bacillus su
294	23	100.0	369	16	Q7VITO	Q7vito helicobacte	367	23	100.0	441	10	Q9C7V2	Q9c7v2 arabidopsis
295	23	100.0	370	16	Q89X19	Q89x19 bradyrhizob	368	23	100.0	441	16	Q9KKE0	Q9kee0 bacillus ha
296	23	100.0	371	2	Q8K2M9	Q8kzm9 bacillus su	369	23	100.0	442	16	Q99VY7	Q99vy7 bradyrhizob
297	23	100.0	372	2	Q93LM9	Q93lm9 cytophaga j	370	23	100.0	443	10	Q9MAU6	Q9mau6 arabidopsis
298	23	100.0	372	5	Q01527	Q01527 caenorhabdi	371	23	100.0	443	11	Q8R2X0	Q8r2x0 mus musculu
299	23	100.0	372	16	Q9A3M8	Q9a3m8 caulobacter	372	23	100.0	444	16	Q8XH51	Q8xh51 clostridium
300	23	100.0	374	13	Q7ZTU8	Q7zty8 xenopus lae	373	23	100.0	445	3	Q96WL4	Q96wl4 kluyveromyc
301	23	100.0	378	16	Q8FXG8	Q8fxg8 bruceella su	374	23	100.0	445	16	Q88J68	Q88j68 pseudomonas
302	23	100.0	379	2	Q8K2M2	Q8kjm2 rhizobium l	375	23	100.0	445	16	Q8XFJ0	Q8xfj0 salmonella
303	23	100.0	379	10	Q49391	Q49391 arabidopsis	376	23	100.0	446	5	Q95SK9	Q95sk9 drosophila
304	23	100.0	380	16	Q89Q31	Q89q31 bradyrhizob	377	23	100.0	446	16	O05461	O05461 mycobacteri
305	23	100.0	381	5	Q81OX1	Q81ox1 plasmodium	378	23	100.0	446	16	Q7TVF6	Q7tvf6 mycobacteri
306	23	100.0	383	2	O07269	O07269 mycobacteri	379	23	100.0	447	16	O86673	O86673 streptomyce
307	23	100.0	383	16	Q8VKD8	Q8vkd8 mycobacteri	380	23	100.0	447	17	Q8PFS33	Q8pfs33 methanosarc
308	23	100.0	387	16	Q88RN6	Q88rn6 pseudomonas	381	23	100.0	449	2	Q7WXM2	Q7wxm2 alcaligenes

Q28907 archaeoglob	Q9X4K9 enterococcu	Q82ux4 nitrosomona	Q9a486 caulobacter	Q86z18 neurospora	Q47743 enterococcu	Q83u28 enterococcu	Q81uk7 homo sapien	Q81jp4 plasmodium	Q8cif1 mus musculu	Q39878 hepatitis b	Q81125 hepatitis b	Q39883 hepatitis b	Q9qb56 hepatitis b	Q81121 hepatitis b	Q91528 hepatitis b	Q81117 hepatitis b	Q9qb51 hepatitis b	Q9qb50 hepatitis b	Q82z97 enterococcu	Q9lbq7 enterococcu	Q8rf12 fusobacteri	Q8xk01 proteus vul	Q8bse0 mus musculu	Q80485 arabidopsis	Q12938 brachydanio	Q8ncj3 homo sapien	Q88gn7 pseudomonas	Q96bc4 homo sapien	Q27989 archaeoglob	Q8twd4 methanopyru	Q86vg0 homo sapien	Q95tt9 drosophila	Q8pjs4 xanthomonas	Q8p8c0 xanthomonas	Q52501 burkholderi	Q8sda7 pseudomonas	Q89gp9 bradyrhizob	Q822d7 chlamydophi	Q926p4 chlamydia p	Q9k1x2 chlamydia p	Q9d7p9 mus musculu	Q8p762 xanthomonas	Q9p7l2 schizosacch	Q9nqd6 homo sapien	Q7wuh3 clostridium	Q9pl61 chlamydia m	Q44725 caenorhabdi	Q9nc12 tribolium c	Q851v7 oryza sativ	Q8la77 arabidopsis	Q8guh8 arabidopsis	Q9hia6 thermoplasma	Q7yva0 trypanosoma	Q8avw9 xenopus lae	P96718 bacillus su	Q9c7v2 arabidopsis	Q9kee0 bacillus ha	Q99vy7 bradyrhizob	Q9mau6 arabidopsis	Q8r2x0 mus musculu	Q8xh51 clostridium	Q96wl4 kluyveromyc	Q88j68 pseudomonas	Q8xfj0 salmonella	Q95sk9 drosophila	O05461 mycobacteri	Q7tvf6 mycobacteri	O86673 streptomyce	Q8pfs33 methanosarc	Q7wxm2 alcaligenes
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382	23	100.0	450	16	Q8A246	Q8A246 bacteroides	455	23	100.0	502	16	Q9X8T8	Q9X8T8 streptomyce
383	23	100.0	452	2	Q52018	Q52018 pseudomonas	456	23	100.0	502	16	Q06585	Q06585 mycobacteri
384	23	100.0	452	10	Q7XR14	Q7XR14 oryza sativ	457	23	100.0	502	16	Q7VEU9	Q7VEU9 mycobacteri
385	23	100.0	452	16	Q88EE6	Q88EE6 pseudomonas	458	23	100.0	505	16	Q82FG0	Q82FG0 streptomyce
386	23	100.0	454	13	Q8AWE1	Q8AWE1 brachydania	459	23	100.0	507	2	Q936S5	Q936S5 pseudomonas
387	23	100.0	455	5	Q8IMX2	Q8IMX2 drosophila	460	23	100.0	507	5	Q9VUH7	Q9VUH7 drosophila
388	23	100.0	457	16	Q8UGN7	Q8UGN7 agrobacteri	461	23	100.0	507	11	Q8KOE5	Q8KOE5 mus musculu
389	23	100.0	458	10	Q9AYL9	Q9AYL9 oryza sativ	462	23	100.0	508	5	Q9V3W1	Q9V3W1 drosophila
390	23	100.0	458	10	Q8GR13	Q8GR13 oryza sativ	463	23	100.0	508	5	Q8IGL2	Q8IGL2 drosophila
391	23	100.0	458	10	Q7XBZ0	Q7XBZ0 oryza sativ	464	23	100.0	509	16	Q8DOL7	Q8DOL7 yersinia pe
392	23	100.0	458	16	Q9RU65	Q9RU65 deinococcus	465	23	100.0	510	17	Q9Y9C5	Q9Y9C5 aeropyrum p
393	23	100.0	459	16	Q82YF7	Q82YF7 listeria in	466	23	100.0	512	16	Q98N17	Q98N17 rhizobium l
394	23	100.0	459	16	Q8Y3Y5	Q8Y3Y5 listeria mo	467	23	100.0	513	16	Q8E8Q5	Q8E8Q5 shewanella
395	23	100.0	461	10	Q9ZTU6	Q9ZTU6 triticum ae	468	23	100.0	513	17	Q8PZM0	Q8PZM0 methanosarc
396	23	100.0	461	5	Q8IP18	Q8IP18 drosophila	469	23	100.0	518	16	Q91369	Q91369 pseudomonas
397	23	100.0	464	10	Q48933	Q48933 thlaspi goe	470	23	100.0	519	4	Q96HH7	Q96HH7 homo sapien
398	23	100.0	464	17	Q29407	Q29407 archaeoglob	471	23	100.0	519	11	Q8CCL7	Q8CCL7 mus musculu
399	23	100.0	465	8	Q8MA13	Q8MA13 galdieria s	472	23	100.0	520	4	Q8TC50	Q8TC50 homo sapien
400	23	100.0	465	8	Q8LW21	Q8LW21 galdieria s	473	23	100.0	522	9	Q9G0H1	Q9G0H1 roseophaga
401	23	100.0	467	10	Q8H846	Q8H846 oryza sativ	474	23	100.0	522	16	Q8VH27	Q8VH27 brucella me
402	23	100.0	467	11	Q8VH50	Q8VH50 mus musculu	475	23	100.0	523	5	Q9VP67	Q9VP67 drosophila
403	23	100.0	467	11	Q8R3D6	Q8R3D6 mus musculu	476	23	100.0	523	5	Q95U04	Q95U04 drosophila
404	23	100.0	467	16	Q8Z621	Q8Z621 salmonella	477	23	100.0	524	10	Q9LMC8	Q9LMC8 arabisdopsis
405	23	100.0	467	16	Q8Z7V7	Q8Z7V7 salmonella	478	23	100.0	527	5	Q95QZ7	Q95QZ7 caenorhabdi
406	23	100.0	469	2	Q8RQU8	Q8RQU8 corynebacte	479	23	100.0	527	5	Q01894	Q01894 caenorhabdi
407	23	100.0	469	2	Q9Z466	Q9Z466 corynebacte	480	23	100.0	527	16	Q8VNG9	Q8VNG9 anabaena sp
408	23	100.0	469	5	Q8MMK2	Q8MMK2 dugesia jap	481	23	100.0	529	5	Q962K8	Q962K8 plasmodium
409	23	100.0	469	11	Q8C2R1	Q8C2R1 mus musculu	482	23	100.0	529	5	Q96909	Q96909 plasmodium
410	23	100.0	469	16	Q8NTE1	Q8NTE1 corynebacte	483	23	100.0	529	5	Q95QZ8	Q95QZ8 caenorhabdi
411	23	100.0	470	9	Q9AZ00	Q9AZ00 bacterioph	484	23	100.0	529	5	Q95QZ9	Q95QZ9 caenorhabdi
412	23	100.0	474	16	Q8CQ32	Q8CQ32 staphylococ	485	23	100.0	533	5	Q9NLB8	Q9NLB8 plasmodium
413	23	100.0	475	13	Q8AVY8	Q8AVY8 xenopus lae	486	23	100.0	533	13	Q7ZUE0	Q7ZUE0 brachydania
414	23	100.0	475	16	Q8FNE6	Q8FNE6 corynebacte	487	23	100.0	533	16	Q8EG41	Q8EG41 shewanella
415	23	100.0	475	17	Q8TW00	Q8TW00 methanopyru	488	23	100.0	534	5	Q8T6T0	Q8T6T0 drosophila
416	23	100.0	479	16	Q8FSK7	Q8FSK7 corynebacte	489	23	100.0	534	5	Q8IGN0	Q8IGN0 drosophila
417	23	100.0	480	16	Q8AOG3	Q8AOG3 bacteroides	490	23	100.0	534	10	Q9SIL5	Q9SIL5 arabisdopsis
418	23	100.0	481	3	Q42651	Q42651 schizosacch	491	23	100.0	535	11	Q8R491	Q8R491 rattus norv
419	23	100.0	481	16	Q83H68	Q83H68 tropheryma	492	23	100.0	535	11	Q8K590	Q8K590 mus musculu
420	23	100.0	481	16	Q83FF1	Q83FF1 tropheryma	493	23	100.0	535	16	Q8ERE8	Q8ERE8 oceanobacil
421	23	100.0	482	10	Q9PK89	Q9PK89 arabisdopsis	494	23	100.0	536	16	Q7VHQ0	Q7VHQ0 helicobacte
422	23	100.0	482	16	Q83MS0	Q83MS0 tropheryma	495	23	100.0	537	11	Q8R3Z8	Q8R3Z8 rattus norv
423	23	100.0	483	10	Q8S642	Q8S642 oryza sativ	496	23	100.0	537	11	Q8K0B2	Q8K0B2 mus musculu
424	23	100.0	483	16	Q9ACW7	Q9ACW7 caulobacter	497	23	100.0	537	13	Q7ZXE8	Q7ZXE8 xenopus lae
425	23	100.0	484	16	Q9CFK5	Q9CFK5 pasteurella	498	23	100.0	538	5	Q8T3D7	Q8T3D7 caenorhabdi
426	23	100.0	484	16	Q25055	Q25055 helicobacte	499	23	100.0	538	10	Q8H2Q3	Q8H2Q3 oryza sativ
427	23	100.0	484	16	Q9ZMF7	Q9ZMF7 helicobacte	500	23	100.0	538	13	Q7SYA1	Q7SYA1 xenopus lae
428	23	100.0	485	4	Q8UW78	Q8UW78 homo sapien	501	23	100.0	540	5	Q9UXZ2	Q9UXZ2 caenorhabdi
429	23	100.0	485	6	Q9GLN8	Q9GLN8 pan troglod	502	23	100.0	540	5	Q8T8W3	Q8T8W3 drosophila
430	23	100.0	485	6	Q9GLP7	Q9GLP7 pan troglod	503	23	100.0	541	11	Q8R3Z7	Q8R3Z7 rattus norv
431	23	100.0	485	6	Q9GLP6	Q9GLP6 gorilla gor	504	23	100.0	543	4	Q96CB6	Q96CB6 homo sapien
432	23	100.0	486	6	Q9TSZ0	Q9TSZ0 callithrix	505	23	100.0	543	11	Q8BL28	Q8BL28 mus musculu
433	23	100.0	488	16	Q83CM5	Q83CM5 coxiella bu	506	23	100.0	543	11	Q8BH64	Q8BH64 mus musculu
434	23	100.0	489	11	Q8K3A8	Q8K3A8 mus musculu	507	23	100.0	545	16	Q8ZE13	Q8ZE13 yersinia pe
435	23	100.0	490	12	Q91B79	Q91B79 lasa virus	508	23	100.0	546	4	Q8N514	Q8N514 homo sapien
436	23	100.0	490	12	Q91M18	Q91M18 lasa virus	509	23	100.0	548	11	Q7TPR6	Q7TPR6 mus musculu
437	23	100.0	490	12	Q91MJ0	Q91MJ0 lasa virus	510	23	100.0	548	16	Q9KSV7	Q9KSV7 vibrio chol
438	23	100.0	491	11	Q8K0R1	Q8K0R1 mus musculu	511	23	100.0	548	16	Q87QB3	Q87QB3 vibrio para
439	23	100.0	491	12	Q9DQX8	Q9DQX8 lasa virus	512	23	100.0	549	2	Q84CG8	Q84CG8 actinobacil
440	23	100.0	492	16	Q9K4K3	Q9K4K3 streptomyce	513	23	100.0	549	16	Q97M33	Q97M33 clostridium
441	23	100.0	493	16	Q9JSD2	Q9JSD2 chlamydia p	514	23	100.0	550	11	Q8OZZ0	Q8OZZ0 mus musculu
442	23	100.0	493	16	Q9Z7V6	Q9Z7V6 chlamydia p	515	23	100.0	551	13	Q918S6	Q918S6 oncorhynch
443	23	100.0	494	5	Q9W072	Q9W072 drosophila	516	23	100.0	551	13	Q9PT16	Q9PT16 oncorhynch
444	23	100.0	494	16	Q8T460	Q8T460 drosophila	517	23	100.0	551	16	Q89ST6	Q89ST6 bradyrhizob
445	23	100.0	494	16	Q8R9B3	Q8R9B3 thermoanaer	518	23	100.0	551	16	Q7VI63	Q7VI63 helicobacte
446	23	100.0	495	5	Q8T3D5	Q8T3D5 caenorhabdi	519	23	100.0	552	16	Q8U6U6	Q8U6U6 agrobacteri
447	23	100.0	496	5	Q94919	Q94919 drosophila	520	23	100.0	553	16	Q8B8Z1	Q8B8Z1 vibrio vuln
448	23	100.0	496	16	Q7UUF5	Q7UUF5 rhodospirill	521	23	100.0	554	10	Q9LU28	Q9LU28 arabisdopsis
449	23	100.0	500	2	Q8RN29	Q8RN29 campylobact	522	23	100.0	554	11	Q9JHT9	Q9JHT9 mus musculu
450	23	100.0	500	2	Q8RJJ3	Q8RJJ3 campylobact	523	23	100.0	554	11	Q8CQ03	Q8CQ03 mus musculu
451	23	100.0	500	16	Q9PMB6	Q9PMB6 campylobact	524	23	100.0	555	5	Q86S80	Q86S80 caenorhabdi
452	23	100.0	500	17	Q8PUX0	Q8PUX0 methanosarc	525	23	100.0	556	10	Q9AWJ9	Q9AWJ9 oryza sativ
453	23	100.0	501	16	Q8G0T1	Q8G0T1 brucella su	526	23	100.0	556	11	Q8K1X5	Q8K1X5 mus musculu
454	23	100.0	502	2	Q8GPY3	Q8GPY3 pseudomonas	527	23	100.0	561	11	Q8CHI9	Q8CHI9 rattus norv



528	23	100.0	563	16	Q82U87	Q82u87 nitrosomona	601	23	100.0	696	5	Q8T021	Q8t021 drosophila
529	23	100.0	564	10	Q8RXV6	Q8rxv6 arabidopsis	602	23	100.0	699	16	Q8YC56	Q8yc56 bruceella me
530	23	100.0	565	10	Q8S551	Q8s551 cornus seri	603	23	100.0	699	16	Q8FW70	Q8fw70 bruceella su
531	23	100.0	566	11	Q8C9R0	Q8c9r0 mus musculu	604	23	100.0	702	16	Q8XDB2	Q8xdb2 escherichia
532	23	100.0	567	16	Q53377	Q53377 mycobacteri	605	23	100.0	702	16	Q8FJ88	Q8fj88 escherichia
533	23	100.0	570	16	Q7TWD1	Q7twq1 mycobacteri	606	23	100.0	702	16	Q83RX5	Q83rx5 shigella fl
534	23	100.0	575	17	Q97420	Q97420 sulfolobus	607	23	100.0	703	5	Q9NAD6	Q9nad6 caenorhabdi
535	23	100.0	576	5	Q966F0	Q966f0 caenorhabdi	608	23	100.0	703	10	Q9LVA2	Q9lva2 arabidopsis
536	23	100.0	576	10	Q9FGH1	Q9fgl1 arabidopsis	609	23	100.0	706	10	Q8S5J1	Q8s5j1 oryza sativ
537	23	100.0	579	5	Q8SWH4	Q8swh4 encephalito	610	23	100.0	706	16	Q8F5C4	Q8f5c4 leptopiera
538	23	100.0	583	5	Q7YTY5	Q7yty5 drosophila	611	23	100.0	710	4	Q8NSV2	Q8nsv2 homo sapien
539	23	100.0	584	3	Q9P395	Q9p395 neurospora	612	23	100.0	710	11	Q8CHT1	Q8cht1 mus musculu
540	23	100.0	584	3	Q8AE22	Q8ae2 dictyosteli	613	23	100.0	711	16	Q88RL4	Q88rl4 pseudomonas
541	23	100.0	586	10	Q9F1V6	Q9fiv6 arabidopsis	614	23	100.0	712	3	Q9P7F2	Q9p7f2 schizosacch
542	23	100.0	589	5	Q9N5B9	Q9n5b9 caenorhabdi	615	23	100.0	713	4	Q9V253	Q9v253 homo sapien
543	23	100.0	589	11	Q8OYQ4	Q8oyq4 mus musculu	616	23	100.0	714	16	Q8PM66	Q8pm66 xanthomonas
544	23	100.0	590	13	Q7SXV6	Q7sxy6 brachydanio	617	23	100.0	715	10	Q8GUA9	Q8gua9 medicago tr
545	23	100.0	592	5	Q8STB5	Q8stb5 encephalito	618	23	100.0	717	16	Q9PBZ8	Q9pbz8 xyella fas
546	23	100.0	592	11	Q9JLNS	Q9jln5 mus musculu	619	23	100.0	727	16	P96583	P96583 bacillus su
547	23	100.0	596	16	Q8VJ30	Q8vj30 mycobacteri	620	23	100.0	729	10	Q84W64	Q84w64 arabidopsis
548	23	100.0	598	5	Q9W3J9	Q9w3j9 drosophila	621	23	100.0	730	10	O49357	O49357 arabidopsis
549	23	100.0	598	16	Q88AJ0	Q88aj0 pseudomonas	622	23	100.0	732	2	Q46767	Q46767 escherichia
550	23	100.0	599	2	Q9XD73	Q9xd73 streptomyce	623	23	100.0	732	5	Q960C3	Q960c3 drosophila
551	23	100.0	601	16	Q9PMS1	Q9pms1 campylobact	624	23	100.0	732	5	Q8RXT2	Q8rxt2 arabidopsis
552	23	100.0	603	11	Q99K43	Q99k43 mus musculu	625	23	100.0	734	5	Q8I273	Q8i273 plasmodium
553	23	100.0	605	5	Q8SZP3	Q8szp3 drosophila	626	23	100.0	734	16	Q8XC66	Q8xc66 oceanobacil
554	23	100.0	606	16	Q8F8Y9	Q8f8y9 leptospira	627	23	100.0	738	16	Q7XR26	Q7xr26 oryza sativ
555	23	100.0	607	5	Q8T3D6	Q8t3d6 caenorhabdi	628	23	100.0	738	10	Q7XR26	Q7xr26 oryza sativ
556	23	100.0	608	5	Q9SVB7	Q9svb7 schistosoma	629	23	100.0	739	12	Q91WA0	Q91wa0 pothos late
557	23	100.0	610	5	Q9GZJ8	Q9gzj8 bombyx mori	630	23	100.0	740	12	Q84831	Q84831 pothos late
558	23	100.0	613	5	Q8WSPL	Q8wsp1 caenorhabdi	631	23	100.0	741	10	Q9LNO1	Q9ln01 arabidopsis
559	23	100.0	614	16	Q9ABQ4	Q9abq4 caulobacter	632	23	100.0	742	5	Q9N8X0	Q9n8x0 trypanosoma
560	23	100.0	620	11	Q923H2	Q923h2 mus musculu	633	23	100.0	747	10	Q9C5F1	Q9c5f1 arabidopsis
561	23	100.0	622	16	Q892Z0	Q892z0 clostridium	634	23	100.0	748	16	Q87D66	Q87d66 xyella fas
562	23	100.0	623	4	Q9H2G3	Q9h2g3 homo sapien	635	23	100.0	750	16	Q9LVNO	Q9lvn0 arabidopsis
563	23	100.0	624	16	Q8CJL4	Q8cjl4 streptomyce	636	23	100.0	750	16	Q9L328	Q9l328 salmonella
564	23	100.0	625	5	Q8EBQ6	Q8ebq6 drosophila	637	23	100.0	751	10	Q8Z6H1	Q8z6h1 salmonella
565	23	100.0	625	16	Q9CDJ2	Q9cdj2 lactococcus	638	23	100.0	752	4	Q7Z6K8	Q7z6k8 homo sapien
566	23	100.0	628	16	Q7VH11	Q7vhl1 helicobacte	639	23	100.0	752	10	Q43559	Q43559 medicago sa
567	23	100.0	629	16	Q826N5	Q826n5 streptomyce	640	23	100.0	752	16	Q9K109	Q9k109 neisseria m
568	23	100.0	630	4	Q9NVH8	Q9nvh8 homo sapien	641	23	100.0	752	16	Q9J8W8	Q9j8w8 neisseria m
569	23	100.0	631	16	Q8E9Z4	Q8e9z4 shewanella	642	23	100.0	753	10	Q9FGT9	Q9fgt9 arabidopsis
570	23	100.0	635	5	Q9V3G6	Q9v3g6 drosophila	643	23	100.0	753	16	Q8XEL2	Q8xel2 escherichia
571	23	100.0	638	16	Q9W2R9	Q9w2r9 drosophila	644	23	100.0	753	16	Q8FHL1	Q8fhl1 escherichia
572	23	100.0	639	16	Q8XP76	Q8xp76 clostridium	645	23	100.0	753	16	Q7UCI4	Q7uci4 shigella fl
573	23	100.0	641	4	O60311	O60311 homo sapien	646	23	100.0	755	16	Q9G7P8	Q9g7p8 bifidobacte
574	23	100.0	642	16	Q8BLH0	Q8blh0 pseudomonas	647	23	100.0	763	10	Q9FZ11	Q9fz11 arabidopsis
575	23	100.0	650	4	Q9NZF0	Q9nzf0 homo sapien	648	23	100.0	763	10	Q7Y208	Q7y208 arabidopsis
576	23	100.0	652	12	O41929	O41929 murid herpe	649	23	100.0	764	10	Q8L5B2	Q8l5b2 chenopodium
577	23	100.0	654	5	Q9W359	Q9w359 drosophila	650	23	100.0	765	10	Q42651	Q42651 beta vulgar
578	23	100.0	660	13	Q7ZXT2	Q7zxt2 xenopus lae	651	23	100.0	766	10	Q43797	Q43797 nicotiana t
579	23	100.0	667	13	Q7ZWX1	Q7zwx1 xenopus lae	652	23	100.0	768	16	Q98LW9	Q98lw9 rhizobium l
580	23	100.0	668	4	Q9H950	Q9h950 homo sapien	653	23	100.0	768	16	P94866	P94866 leuconostoc
581	23	100.0	668	16	Q9CF31	Q9cf31 lactococcus	654	23	100.0	772	2	Q94866	Q94866 leuconostoc
582	23	100.0	668	16	Q9H950	Q9h950 homo sapien	655	23	100.0	773	5	Q95TR3	Q95tr3 drosophila
583	23	100.0	668	16	Q9H950	Q9h950 homo sapien	656	23	100.0	773	10	Q94CP2	Q94cp2 oryza sativ
584	23	100.0	670	4	Q9H950	Q9h950 homo sapien	657	23	100.0	773	10	Q7XAC0	Q7xac0 oryza sativ
585	23	100.0	676	5	Q24085	Q24085 drosophila	658	23	100.0	780	16	Q8XK07	Q8xk07 bradyrhizob
586	23	100.0	676	5	Q95SQ4	Q95sq4 drosophila	659	23	100.0	783	16	Q8YC67	Q8yc67 bruceella me
587	23	100.0	676	5	Q7YZQ2	Q7yzq2 bactroera	660	23	100.0	783	16	Q8FW59	Q8fw59 bruceella su
588	23	100.0	677	5	Q9GYN2	Q9gyn2 caenorhabdi	661	23	100.0	784	16	Q8UFU4	Q8ufu4 agrobacteri
589	23	100.0	681	2	Q91U51	Q91u51 rhizobium m	662	23	100.0	785	5	Q86S21	Q86s21 caenorhabdi
590	23	100.0	681	16	Q9M388	Q9m388 bradyrhizob	663	23	100.0	785	16	Q7VN79	Q7vn79 haemophilus
591	23	100.0	685	10	Q9SR82	Q9sr82 arabidopsis	664	23	100.0	786	5	Q9N5B7	Q9n5b7 caenorhabdi
592	23	100.0	685	16	Q9ML54	Q9ml54 rhizobium l	665	23	100.0	786	16	Q97M65	Q97m65 clostridium
593	23	100.0	686	5	Q8MOP5	Q8mr5 drosophila	666	23	100.0	787	5	Q9TZD9	Q9tzd9 caenorhabdi
594	23	100.0	686	10	Q9SUF9	Q9suf9 arabidopsis	667	23	100.0	787	10	Q9SZJ2	Q9szj2 arabidopsis
595	23	100.0	688	10	Q9J8K8	Q9j8k8 arabidopsis	668	23	100.0	789	10	Q8S1W8	Q8s1w8 oryza sativ
596	23	100.0	688	10	Q93Y56	Q93ys6 arabidopsis	669	23	100.0	789	16	Q92QM0	Q92qm0 rhizobium m
597	23	100.0	688	16	Q88D17	Q88d17 pseudomonas	670	23	100.0	791	5	Q81SG8	Q81sg8 stylonychia
598	23	100.0	690	5	Q95XR4	Q95xr4 caenorhabdi	671	23	100.0	791	5	Q86CV7	Q86cv7 stylonychia
599	23	100.0	694	11	Q9JUN0	Q9jin0 mus musculu	672	23	100.0	791	16	Q9JZB6	Q9jzb6 neisseria m
600	23	100.0	696	5	Q9VUZ6	Q9vuz6 drosophila	673	23	100.0	791	16	Q9JUD1	Q9jud1 neisseria m

674	23	100.0	793	5	Q9VXP5	Q9vxp5 drosophila	747	23	100.0	1032	10	Q38766	Q38766 avena sativ
675	23	100.0	793	10	Q9LXK67	Q9lck67 arabidopsis	748	23	100.0	1039	5	Q9GV97	Q9gv97 toxoplasma
676	23	100.0	800	16	Q9CJP2	Q9cjp2 pasteurella	749	23	100.0	1051	11	Q91XT4	Q91xt4 mus musculus
677	23	100.0	802	4	Q9H998	Q9h998 homo sapien	750	23	100.0	1051	11	Q91XT4	Q91xt4 mus musculus
678	23	100.0	803	1	Q87780	Q87780 pyrobaculum	751	23	100.0	1058	11	Q925T1	Q925t1 rattus norv
679	23	100.0	803	17	Q97UH8	Q97uh8 sulfolobus	752	23	100.0	1075	5	Q9NC90	Q9nc90 strongyloce
680	23	100.0	806	16	Q7WXX6	Q7wxx6 bordetella	753	23	100.0	1085	16	Q7U243	Q7u243 mycobacteri
681	23	100.0	807	16	Q8PAG7	Q8pag7 xanthomonas	754	23	100.0	1092	16	Q53720	Q53720 mycobacteri
682	23	100.0	809	10	Q8RWQ1	Q8rwi1 arabidopsis	755	23	100.0	1111	10	Q9FZ10	Q9fz10 arabidopsis
683	23	100.0	810	16	Q69650	Q69650 mycobacteri	756	23	100.0	1116	16	Q97KU3	Q97ku3 clostridium
684	23	100.0	810	16	Q7TVY3	Q7tvv3 mycobacteri	757	23	100.0	1123	16	Q89VS9	Q89vs9 bradyrhizob
685	23	100.0	812	16	Q8XFE8	Q8xf8 salmonella	758	23	100.0	1130	11	Q80TZ5	Q80tz5 mus musculu
686	23	100.0	814	11	Q9L749	Q9l749 arabidopsis	759	23	100.0	1131	5	Q9VLM2	Q9v1w2 drosophila
687	23	100.0	817	11	Q91YT6	Q91yt6 mus musculu	760	23	100.0	1135	10	Q7XSG9	Q7xe9 oryza sativ
688	23	100.0	817	16	Q8DCT9	Q8dct9 vibrio vuln	761	23	100.0	1145	10	Q8GUE7	Q8gue7 cymodocea n
689	23	100.0	820	16	Q8AAE0	Q8aae0 bacteroides	762	23	100.0	1148	10	Q8H97	Q8h97 oryza sativ
690	23	100.0	822	3	Q9P312	Q9p312 neurospora	763	23	100.0	1157	5	Q27088	Q27088 trichomonas
691	23	100.0	826	16	Q7WTI8	Q7wti8 bordetella	764	23	100.0	1157	5	Q27088	Q27088 trichomonas
692	23	100.0	826	16	Q7VTK5	Q7vtx5 bordetella	765	23	100.0	1162	5	Q24818	Q24818 entamoeba h
693	23	100.0	827	16	Q8XDL9	Q8xdl9 escherichia	766	23	100.0	1165	5	Q24860	Q24860 entamoeba h
694	23	100.0	827	16	Q8FAK5	Q8fak5 escherichia	767	23	100.0	1170	16	Q7VBU2	Q7vbu2 prochloroco
695	23	100.0	827	16	Q8D6Y1	Q8d6y1 vibrio vuln	768	23	100.0	1180	5	Q3VPV5	Q3vpv5 drosophila
696	23	100.0	834	10	Q9SVA5	Q9sva5 arabidopsis	769	23	100.0	1191	5	Q9XYX3	Q9xyx3 dictyosteli
697	23	100.0	835	5	Q9NSE8	Q9ns8 caenorhabdi	770	23	100.0	1193	16	Q7V7H1	Q7v7h1 prochloroco
698	23	100.0	837	2	Q93DI1	Q93dl1 acinetobact	771	23	100.0	1196	5	Q23866	Q23866 dictyosteli
699	23	100.0	838	5	Q9GQV1	Q9gd1 acinetobact	772	23	100.0	1199	10	Q84R14	Q84r14 arabidopsis
700	23	100.0	844	16	Q8CVF4	Q8cvf4 leptospira	773	23	100.0	1215	5	Q9W2K4	Q9w2k4 drosophila
701	23	100.0	844	16	Q83DI2	Q83di2 acinetobact	774	23	100.0	1226	5	Q9V4U3	Q9v4u3 drosophila
702	23	100.0	844	16	Q82TV5	Q82tv5 yersinia pe	775	23	100.0	1230	10	Q8RU68	Q8ru68 oryza sativ
703	23	100.0	857	16	Q88DE6	Q88de6 pseudomonas	776	23	100.0	1235	5	Q8IEN8	Q8ien8 plasmodium
704	23	100.0	865	10	Q9FZB2	Q9fzb2 arabidopsis	777	23	100.0	1249	11	Q80TH4	Q80th4 mus musculu
705	23	100.0	865	16	Q8X957	Q8x957 escherichia	778	23	100.0	1254	13	Q7SYD5	Q7syd5 bradydiano
706	23	100.0	865	16	Q7UDR9	Q7udr9 shigella fl	779	23	100.0	1256	16	Q8DRA6	Q8dra6 streptococc
707	23	100.0	867	10	Q8GZ28	Q8gr28 arabidopsis	780	23	100.0	1257	4	Q43738	Q43738 homo sapien
708	23	100.0	871	16	Q9PZ11	Q9pzi1 campylobact	781	23	100.0	1257	11	Q9Z301	Q9z301 rattus norv
709	23	100.0	872	5	Q8MZH3	Q8mzh3 drosophila	782	23	100.0	1258	5	Q8T6L6	Q8t6l6 drosophila
710	23	100.0	872	5	Q9VGU5	Q9vgu5 drosophila	783	23	100.0	1264	5	Q9V4U4	Q9v4u4 drosophila
711	23	100.0	872	11	Q8KOB3	Q8kob3 mus musculu	784	23	100.0	1267	3	Q8JOT2	Q8jot2 emericeila
712	23	100.0	874	16	Q8DAR2	Q8dar2 vibrio vuln	785	23	100.0	1267	3	Q8JOT2	Q8jot2 emericeila
713	23	100.0	876	2	Q32739	Q32739 clostridium	786	23	100.0	1269	5	Q22855	Q22855 caenorhabdi
714	23	100.0	876	2	Q9KHA1	Q9kha1 clostridium	787	23	100.0	1278	5	Q8T6L7	Q8t6l7 drosophila
715	23	100.0	876	16	Q87QX7	Q87qx7 vibrio para	788	23	100.0	1280	16	Q978SQ7	Q97sq7 streptococc
716	23	100.0	877	16	Q87VK1	Q87vk1 pseudomonas	789	23	100.0	1287	5	Q9F930	Q9f930 streptococc
717	23	100.0	879	2	Q06498	Q06498 clostridium	790	23	100.0	1287	5	Q7YTV8	Q7yrv8 drosophila
718	23	100.0	883	9	Q858N4	Q858n4 yersinia pe	791	23	100.0	1302	4	Q9H582	Q9h582 homo sapien
719	23	100.0	884	9	Q9T145	Q9t145 bacterioph	792	23	100.0	1304	5	Q9U3L2	Q9u3l2 caenorhabdi
720	23	100.0	891	5	Q21853	Q21853 caenorhabdi	793	23	100.0	1314	16	Q82BJ3	Q82bj3 streptomyc
721	23	100.0	891	5	Q86B99	Q86b99 drosophila	794	23	100.0	1326	5	Q22240	Q22240 caenorhabdi
722	23	100.0	893	5	Q9WLS3	Q9wls3 drosophila	795	23	100.0	1345	16	Q8Y282	Q8y282 raltstonia s
723	23	100.0	898	5	Q9VDK3	Q9vdk3 drosophila	796	23	100.0	1355	16	Q8XXK6	Q8xxk6 clostridium
724	23	100.0	915	5	Q9VDK3	Q9vdk3 drosophila	797	23	100.0	1356	5	Q8TKX7	Q8tkx7 drosophila
725	23	100.0	916	16	Q8FL11	Q8fl11 escherichia	798	23	100.0	1421	10	Q84ZK6	Q84zr6 oryza sativ
726	23	100.0	916	16	Q83SM4	Q83sm4 shigella fl	799	23	100.0	1431	11	Q8K3T7	Q8k3t7 mus musculu
727	23	100.0	940	10	Q81502	Q81502 arabidopsis	800	23	100.0	1431	3	Q8TFI7	Q8tfi7 saccharomyc
728	23	100.0	942	2	Q938A0	Q938a0 mycobacteri	801	23	100.0	1445	4	Q9ULL6	Q9ull6 homo sapien
729	23	100.0	955	4	Q81ZQ4	Q81zq4 homo sapien	802	23	100.0	1462	3	Q42874	Q42874 schizosacch
730	23	100.0	955	4	Q7Z4H7	Q7z4h7 homo sapien	803	23	100.0	1508	16	Q9A2F8	Q9a2f8 caulobacter
731	23	100.0	955	5	Q20829	Q20829 caenorhabdi	804	23	100.0	1526	5	Q94538	Q94538 drosophila
732	23	100.0	960	16	Q8XWL6	Q8xwl6 raltstonia s	805	23	100.0	1526	5	Q94538	Q94538 drosophila
733	23	100.0	963	1	Q977Q8	Q977q8 uncultured	806	23	100.0	1548	5	Q9V6D5	Q9v6d5 drosophila
734	23	100.0	967	16	Q8FVJ5	Q8fvj5 brucella su	807	23	100.0	1548	5	Q9NE01	Q9ne01 leishmania
735	23	100.0	976	16	Q9AB92	Q9ab92 caulobacter	808	23	100.0	1556	5	Q9VRP1	Q9vrp1 drosophila
736	23	100.0	979	11	Q9EP71	Q9ep71 mus musculu	809	23	100.0	1573	5	Q9VMF3	Q9vmf3 drosophila
737	23	100.0	982	5	Q81DQ6	Q81dq6 plasmodium	810	23	100.0	1573	5	Q95V18	Q95v18 drosophila
738	23	100.0	987	11	Q8K166	Q8k166 mus musculu	811	23	100.0	1586	5	Q18798	Q18798 caenorhabdi
739	23	100.0	992	11	Q7TT14	Q7tt14 mus musculu	812	23	100.0	1590	5	Q8MX30	Q8mx30 naegleria g
740	23	100.0	998	17	Q8RHF6	Q8rhf6 mechanosarc	813	23	100.0	1599	9	Q854N0	Q854n0 mycobacteri
741	23	100.0	999	11	Q8BR49	Q8br49 mus musculu	814	23	100.0	1628	16	Q9EQZ7	Q9eqz7 mycoplasma
742	23	100.0	1007	5	Q9VAE4	Q9vae4 drosophila	815	23	100.0	1750	10	Q9LPC5	Q9lpc5 arabidopsis
743	23	100.0	1026	11	Q9QZY0	Q9qzy0 mus musculu	816	23	100.0	1751	5	Q17143	Q17143 drosophila
744	23	100.0	1027	4	Q86VS3	Q86vs3 homo sapien	817	23	100.0	1756	10	Q80975	Q80975 arabidopsis
745	23	100.0	1027	4	Q86VS3	Q86vs3 homo sapien	818	23	100.0	1773	5	Q17142	Q17142 drosophila
746	23	100.0	1028	16	Q9CMN0	Q9cmn0 pasteurella	819	23	100.0	1776	5	Q9V6E1	Q9v6e1 drosophila

820	23	100.0	1803	5	Q8MLG1	Q8mlg1 drosophila	893	20	87.0	82	16	Q8UDB5	Q8udb5 agrobacteri
821	23	100.0	1844	5	Q8IE31	Q8ie31 plasmodium	894	20	87.0	83	16	Q8NN4	Q8enn4 rhizobium l
822	23	100.0	1869	5	Q8IC11	Q8ic11 plasmodium	895	20	87.0	84	5	Q45190	Q45190 caenorhabdi
823	23	100.0	1869	5	Q86N11	Q86n11 caenorhabdi	896	20	87.0	84	16	Q8Y190	Q8y190 brucella me
824	23	100.0	1917	4	Q8H1I9	Q8h1i9 homo sapien	897	20	87.0	84	16	Q8FZM6	Q8fzm6 brucella su
825	23	100.0	1956	4	Q43154	Q43154 homo sapien	898	20	87.0	85	2	Q8RPH8	Q8rph8 desulfitoba
826	23	100.0	1980	12	Q991N2	Q991n2 little cher	899	20	87.0	86	10	Q9FEL4	Q9fel4 nicotiana t
827	23	100.0	2010	5	Q19330	Q19330 caenorhabdi	900	20	87.0	87	10	Q8GV19	Q8gv19 nicotiana a
828	23	100.0	2061	5	Q77025	Q77025 drosophila	901	20	87.0	87	16	Q8DLN4	Q8dlm4 synchococc
829	23	100.0	2062	5	Q8ML45	Q8ml45 drosophila	902	20	87.0	87	16	Q8A46	Q8a46 coxiella bu
830	23	100.0	2138	5	Q9XZE3	Q9xze3 amoeba prot	903	20	87.0	88	16	Q87761	Q87761 mycobacteri
831	23	100.0	2138	5	Q9XZE3	Q9xze3 amoeba prot	904	20	87.0	88	16	Q87761	Q87761 mycobacteri
832	23	100.0	2141	6	Q8WJ04	Q8wj04 canis famil	905	20	87.0	90	2	Q7ULM0	Q7ulm0 mycobacteri
833	23	100.0	2149	6	Q8WJ04	Q8wj04 canis famil	906	20	87.0	90	2	Q7ULM0	Q7ulm0 mycobacteri
834	23	100.0	2152	6	Q8WJ06	Q8wj06 papio hamad	907	20	87.0	91	16	Q53401	Q53401 mycobacteri
835	23	100.0	2154	10	Q9ZVC8	Q9zvc8 arabidopsis	908	20	87.0	91	16	Q7U4S3	Q7u4s3 synchococc
836	23	100.0	2202	4	Q8N3C0	Q8n3c0 homo sapien	909	20	87.0	91	16	Q7U4S3	Q7u4s3 synchococc
837	23	100.0	2205	5	Q8MLG2	Q8mlg2 drosophila	910	20	87.0	91	16	Q7U4S3	Q7u4s3 synchococc
838	23	100.0	2210	5	Q9GV2	Q9gv2 drosophila	911	20	87.0	91	16	Q7U4S3	Q7u4s3 synchococc
839	23	100.0	2284	5	Q815Y7	Q815y7 plasmodium	912	20	87.0	95	10	Q39984	Q39984 hordeum bog
840	23	100.0	2294	5	Q9VUB7	Q9vub7 drosophila	913	20	87.0	95	10	Q39976	Q39976 hordeum lec
841	23	100.0	2370	5	Q9VEN1	Q9ven1 drosophila	914	20	87.0	95	10	Q39976	Q39976 hordeum lec
842	23	100.0	2408	5	Q8S484	Q8s484 zea mays (m	915	20	87.0	95	10	Q39971	Q39971 hordeum chi
843	23	100.0	2430	11	Q55140	Q55140 mus musculu	916	20	87.0	95	16	Q7UUX7	Q7uux7 rhizobium l
844	23	100.0	2437	11	Q83725	Q83725 rattus norv	917	20	87.0	95	16	Q7UUX7	Q7uux7 rhizobium l
845	23	100.0	2555	5	Q8T9E3	Q8t9e3 drosophila	918	20	87.0	98	13	Q8QGA7	Q8qga7 oncorhynch
846	23	100.0	2559	5	Q44381	Q44381 drosophila	919	20	87.0	99	16	Q49504	Q49504 mycoplasma
847	23	100.0	2559	5	Q44113	Q44113 drosophila	920	20	87.0	99	16	Q7VUF5	Q7vuf5 helicobacte
848	23	100.0	2559	5	Q9V7X3	Q9v7x3 drosophila	921	20	87.0	101	2	Q86936	Q86936 acinetobact
849	23	100.0	2615	16	Q9CPI1	Q9cpil pasteurella	922	20	87.0	103	10	Q8LNP7	Q8lnp7 oryza sativ
850	23	100.0	2664	6	Q8WN95	Q8wn95 bos taurus	923	20	87.0	104	10	Q851K8	Q851k8 oryza sativ
851	23	100.0	2747	5	Q8ICL5	Q8icl5 plasmodium	924	20	87.0	104	11	Q8C8L4	Q8c8l4 mus musculu
852	23	100.0	3074	10	Q9SMH5	Q9smh5 chlamydomon	925	20	87.0	104	11	Q8C8L4	Q8c8l4 mus musculu
853	23	100.0	3111	5	Q9VH10	Q9vh10 drosophila	926	20	87.0	104	11	Q8C8L4	Q8c8l4 mus musculu
854	23	100.0	3225	16	Q9PKM6	Q9pkm6 chlamydia m	927	20	87.0	105	16	Q8Z46	Q8zx46 ralistonia s
855	23	100.0	3268	3	Q03280	Q03280 saccharomyc	928	20	87.0	106	16	Q8D6R0	Q8d6r0 vibrio vuln
856	23	100.0	3268	3	Q8IC30	Q8ic30 plasmodium	929	20	87.0	108	2	Q8NRC9	Q8nrc9 escherichia
857	23	100.0	3269	12	Q777N5	Q777n5 papaya leaf	930	20	87.0	108	16	Q8EDY0	Q8edy0 shewanella
858	23	100.0	3291	12	Q66225	Q66225 cryphonectr	931	20	87.0	110	11	Q64497	Q64497 mus musculu
859	23	100.0	3542	5	Q9Y2F3	Q9y2f3 plasmodium	932	20	87.0	111	5	Q21111	Q21111 caenorhabdi
860	23	100.0	3674	5	Q9TYG9	Q9tyg9 caenorhabdi	933	20	87.0	112	5	Q8T3C4	Q8t3c4 caenorhabdi
861	23	100.0	3674	5	Q9TW65	Q9tw65 caenorhabdi	934	20	87.0	112	17	Q9YEX4	Q9yex4 aeropyrum p
862	23	100.0	3692	16	Q8CNU9	Q8cnu9 staphylococ	935	20	87.0	114	16	Q8KE96	Q8ke96 chlorobium
863	23	100.0	4024	4	Q8WXX0	Q8wx0 homo sapien	936	20	87.0	116	4	Q96DA6	Q96da6 homo sapien
864	23	100.0	4031	4	Q9Y2F3	Q9y2f3 homo sapien	937	20	87.0	116	11	Q9CQV7	Q9cq7 mus musculu
865	23	100.0	4277	5	Q7YVYK3	Q7yv3 trypanosoma	938	20	87.0	116	16	Q837D5	Q837d5 enterococu
866	23	100.0	4861	4	Q15751	Q15751 homo sapien	939	20	87.0	117	3	Q74332	Q74332 schizosacch
867	23	100.0	5106	5	Q9VAV5	Q9vav5 drosophila	940	20	87.0	117	16	Q9ACS9	Q9acs9 streptomyce
868	20	87.0	5106	5	Q8MQB9	Q8mqb9 caenorhabdi	941	20	87.0	117	16	Q82AZ7	Q82az7 streptomyce
869	20	87.0	5106	5	Q8MQB9	Q8mqb9 caenorhabdi	942	20	87.0	118	2	Q936Y7	Q936y7 pseudomonas
870	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	943	20	87.0	118	2	Q936Y7	Q936y7 pseudomonas
871	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	944	20	87.0	121	4	Q8N9K7	Q8n9k7 homo sapien
872	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	945	20	87.0	121	4	Q8N9K7	Q8n9k7 homo sapien
873	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	946	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
874	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	947	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
875	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	948	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
876	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	949	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
877	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	950	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
878	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	951	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
879	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	952	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
880	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	953	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
881	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	954	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
882	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	955	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
883	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	956	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
884	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	957	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
885	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	958	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
886	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	959	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
887	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	960	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
888	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	961	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
889	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	962	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
890	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	963	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
891	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	964	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas
892	20	87.0	5106	5	Q9GTM3	Q9gym3 caenorhabdi	965	20	87.0	122	16	Q9HXL1	Q9hxl1 pseudomonas

966 20 87.0 136 2 069489  
 967 20 87.0 137 4 096AG7  
 968 20 87.0 137 5 093UJ2  
 969 20 87.0 137 16 07VNO2  
 970 20 87.0 138 10 09SMT5  
 971 20 87.0 138 16 08YMO7  
 972 20 87.0 138 16 07UB48  
 973 20 87.0 140 4 09POQ1  
 974 20 87.0 140 10 08LCT5  
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 976 20 87.0 140 11 09C2G9  
 977 20 87.0 140 16 081RG1  
 978 20 87.0 140 16 081EB4  
 979 20 87.0 141 16 08X5P6  
 980 20 87.0 142 16 007579  
 981 20 87.0 143 10 085OW4  
 982 20 87.0 144 16 08FAW1  
 983 20 87.0 145 4 086UJ2  
 984 20 87.0 146 16 0831W4  
 985 20 87.0 147 2 08GNH8  
 986 20 87.0 147 5 07YWS8  
 987 20 87.0 148 2 09XB81  
 988 20 87.0 148 9 003943  
 989 20 87.0 148 16 092X98  
 990 20 87.0 149 4 08NSB8  
 991 20 87.0 149 5 07YTE2  
 992 20 87.0 150 2 054244  
 993 20 87.0 150 16 098J94  
 994 20 87.0 150 16 09X8U9  
 995 20 87.0 150 16 0833X9  
 996 20 87.0 151 16 09HXK3  
 997 20 87.0 151 16 08PK27  
 998 20 87.0 152 3 096U94  
 999 20 87.0 152 5 093141  
 1000 20 87.0 152 16 08P6C3

## ALIGNMENTS

RESULT 1  
 Q9QVS7  
 ID Q9QVS7 PRELIMINARY; PRT; 17 AA.  
 AC Q9QVS7  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
 DE Lactate dehydrogenase-A (Fragment).  
 OS Mus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10095;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95201434; PubMed=7534515;  
 RA Sandulache R., Preusch W., Chatterjee B., Gimbel W., Graw J.,  
 RA Favor J.;  
 RT "Molecular analysis of four lactate dehydrogenase-A mutants in the  
 RT mouse."  
 RL Mamm. Genome 5:777-780(1994).  
 SQ SEQUENCE 17 AA; 1982 MW; E941E0A3F2477D45 CRC64;  
 Query Match 100.0%; Score 23; DB 11; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 58;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 DB 9 DAHK 12

RESULT 2  
 Q9QVA1

ID Q9QVA1 PRELIMINARY; PRT; 21 AA.  
 AC Q9QVA1;  
 DT 01-MAY-2000 (TRENBLrel. 13, Created)  
 DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE 49 kDa protein (Fragment).  
 OS Rattus sp.  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 ON NCBI\_TaxID=10118;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93105636; PubMed=1468220;  
 RA Zhu L., Crouch R.K.;  
 RT "Albumin in the cornea is oxidized by hydrogen peroxide."  
 RL Cornea 11:567-572(1992).  
 DR HSP; P02768; IETH.  
 DR GO; GO:0005615; C:extracellular space; IEA.  
 DR GO; GO:0005386; F:carrier activity; IEA.  
 DR GO; GO:0006810; P:transport; IEA.  
 DR InterPro: IPR000264; Serum\_albumin.  
 DR Pfam: PF00277; transport\_prot; 1.  
 SQ SEQUENCE 21 AA; 2429 MW; 26134A3D7CE29FAC CRC64;  
 Query Match 100.0%; Score 23; DB 11; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 72;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 DB 1 DAHK 4

RESULT 3  
 Q91093

ID Q91093 PRELIMINARY; PRT; 47 AA.  
 AC Q91093;  
 DT 01-NOV-1996 (TRENBLrel. 01, Created)  
 DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)  
 DE Prolactin receptor (Fragment).  
 OS Meleagris gallopavo (Common turkey).  
 OC Archosauria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.  
 ON NCBI\_TaxID=9103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Ovarian small white follicles;  
 RA Pitts G.R., You S.K., Foster D.N., El Halawani M.E.;  
 RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U22946; AAA75040.1;  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER 1  
 FT NON\_TER 47  
 SQ SEQUENCE 47 AA; 5216 MW; 6PE5C9609B39F509 CRC64;

Query Match 100.0%; Score 23; DB 13; Length 47;  
 Best Local Similarity 100.0%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 DB 8 DAHK 11

RESULT 4  
 Q8ZZ28

ID Q8ZZ28 PRELIMINARY; PRT; 50 AA.  
 AC Q8ZZ28;  
 DT 01-MAR-2002 (TRENBLrel. 20, Created)  
 DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)

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DE Hypothetical protein PAE0471.
GN PAE0471.
OS Pyrobaculum aerophilum.
OC Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID=13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IM2 / ATCC 51768 / DSM 7523;
RL MEDLINE=21664397; PubMed=11792869;
RX Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA Miller J.H.;
RT "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
aerophilum.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR EMBL; AE009769; AAL62813.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 50 AA; 5883 MW; 9351DE9C9A5E1A6E CRC64;

Query Match 100.0%; Score 23; DB 17; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4
Db 15 DAHK 18

RESULT 5
Q88VE6 PRELIMINARY; PRT; 56 AA.
AC Q88VE6;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein.
GN LP_2112.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Tarchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Stiekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;
RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 56 AA; 6438 MW; 78C141687E7FF005 CRC64;

Query Match 100.0%; Score 23; DB 16; Length 56;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4
Db 53 DAHK 56

RESULT 6
Q42106 PRELIMINARY; PRT; 59 AA.
AC Q42106;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JAN-1999 (TrEMBLrel. 09, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Protein kinase inhibitor (Fragment).

OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; TISSUE=Seedling;
RA Hofte H.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z26527; CRA81298.1; -.
DR HSSP; P29312; 1A38.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0019904; F:protein domain specific binding; IEA.
DR InterPro; IPR000308; 14-3-3.
DR Pfam; PF00244; 14-3-3; 1.
DR ProDom; PD000600; 14-3-3; 1.
DR PROSITE; PS00797; 1433_2; 1.
KW Kinase.
FT NON TER 1
SQ SEQUENCE 59 AA; 6320 MW; 080C0F25F5A6C889 CRC64;

Query Match 100.0%; Score 23; DB 10; Length 59;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4
Db 41 DAHK 44

RESULT 7
Q91889 PRELIMINARY; PRT; 66 AA.
ID Q91889
AC Q91889;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Somatolactin precursor (Fragment).
OS Oncorhynchus tshawytscha (Chinook salmon) (King salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=74940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VARIOUS STRAINS;
RA Ford M.J.;
RT "Effects of natural selection on patterns of DNA sequence variation at
the transferrin, somatolactin, and p53 genes within and among chinook
salmon (Oncorhynchus tshawytscha) populations.";
RL Mol. Ecol. 9:0-0(2000).
DR EMBL; AF223890; AAF81065.1; -.
DR EMBL; AF223821; AAF81019.1; -.
DR EMBL; AF223824; AAF81021.1; -.
DR EMBL; AF223827; AAF81023.1; -.
DR EMBL; AF223830; AAF81025.1; -.
DR EMBL; AF223833; AAF81027.1; -.
DR EMBL; AF223836; AAF81029.1; -.
DR EMBL; AF223839; AAF81031.1; -.
DR EMBL; AF223842; AAF81033.1; -.
DR EMBL; AF223845; AAF81035.1; -.
DR EMBL; AF223848; AAF81037.1; -.
DR EMBL; AF223851; AAF81039.1; -.
DR EMBL; AF223854; AAF81041.1; -.
DR EMBL; AF223857; AAF81043.1; -.
DR EMBL; AF223860; AAF81045.1; -.
DR EMBL; AF223863; AAF81047.1; -.
DR EMBL; AF223866; AAF81049.1; -.
DR EMBL; AF223869; AAF81051.1; -.
DR EMBL; AF223872; AAF81053.1; -.
DR EMBL; AF223875; AAF81055.1; -.
DR EMBL; AF223878; AAF81057.1; -.

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DR EMBL; AF223881; AAF81059.1; -.
DR EMBL; AF223884; AAF81061.1; -.
DR EMBL; AF223887; AAF81063.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; hormone; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
FT NON TER 1
SQ SEQUENCE 66 AA; 7822 MW; 3CD2A6837C2E359A CRC64;

Query Match 100.0%; Score 23; DB 13; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAKH 4
Db 42 DAKH 45

RESULT 8
Q852W2 PRELIMINARY; PRT; 73 AA.
AC Q852W2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Gp243.
GN 243.
OS Mycobacteriophage Bx21.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=205877;
RN [1]
RP MEDLINE=22592660; PubMed=12705866;
RA Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,
RA Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Pannunzio N.R.,
RA Brucker W., Kumar V., Kandaamy J., Keenan L., Bardarov S.,
RA Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,
RA Hatfull G.F.;
RT "Origins of highly mosaic mycobacteriophage genomes.";
RL Cell 113:171-182(2003).
DR EMBL; AV129337; AAN16875.1; -.
SQ SEQUENCE 73 AA; 8001 MW; 0F08C6D4BB6D241B CRC64;

Query Match 100.0%; Score 23; DB 9; Length 73;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAKH 4
Db 53 DAKH 56

RESULT 9
Q9RON2 PRELIMINARY; PRT; 81 AA.
AC Q9RON2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE LR11 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20027760; PubMed=10559012;
RA Kanaki T., Bujo H., Hirayama S., Ishii I., Morisaki N.,
RA Schneider W.J., Saito Y.;
RT "Expression of LR11, a mosaic LDL receptor family member, is markedly
increased in atherosclerotic lesions.";
RL Arterioscler. Thromb. Vasc. Biol. 19:2687-2695(1999).
DR EMBL; AB026993; BAA86122.1; -.
DR InterPro; IPR008957; FN_III-like.
FT NON TER 1
FT NON TER 81
SQ SEQUENCE 81 AA; 8769 MW; 5E2C718C72EEE013 CRC64;

Query Match 100.0%; Score 23; DB 11; Length 81;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAKH 4
Db 11 DAKH 14

RESULT 10
Q8W6D6 PRELIMINARY; PRT; 82 AA.
AC Q8W6D6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Prim-VSK.
GN ORF82.
OS Vibrio phage VSK.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=181604;
RN [1]
RP SEQUENCE FROM N.A.
RA Basu N., Kar S., Ghosh R.K.;
RT "Molecular analysis of filamentous phage VSK of Vibrio cholerae 0139:
A possible clue to genetic transmission.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF453500; AAL49735.1; -.
SQ SEQUENCE 82 AA; 8933 MW; 32E495E7C265A0A9 CRC64;

Query Match 100.0%; Score 23; DB 9; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAKH 4
Db 52 DAKH 55

RESULT 11
O56843 PRELIMINARY; PRT; 82 AA.
ID O56843;
AC O56843;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Vibrio cholerae O139 fsl phage.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=70203;
RN [1]
RP SEQUENCE FROM N.A.
RA Homma Y.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97457190; PubMed=9311128;
RA Ebara M., Shimodori S., Kojima F., Ichinose Y., Hirayama T.,
RA Albert M.J., Supawat K., Homma Y., Iwanaga M., Amako K.;
RT "Characterization of filamentous phage of Vibrio cholerae O139 and
O1.";
RL FEMS Microbiol. Lett. 154:293-301(1997).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=98201718; PubMed=9540841;

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RA	Homma Y., Ikema M., Toma C., Ehara M., Iwanaga M.;	DR	GO: 0016829; F-lyase activity; IEA.
RT	"Molecular analysis of a filamentous phage (fsl) of Vibrio cholerae	DR	GO: 0008270; F-zinc ion binding; IEA.
RT	O139.";	DR	GO: 0006096; P-glycolysis; IEA.
RL	Biochim. Biophys. Acta 1362:109-115(1997).	DR	InterPro; IPR000771; K_bp_aldolase.
DR	EMBL: D89074; BAA24170.1; -	DR	Pfam; PF01116; F_bp_aldolase; 1.
KW	Hypothetical protein.	DR	ProDom; PD002376; K_bp_aldolase; 1.
SQ	SEQUENCE 82 AA; 8928 MW; B11D180214634BB3 CRC64;	FT	NON TER 84 84
		SQ	SEQUENCE 84 AA; 9422 MW; C8B61DB0474EB906 CRC64;
Query Match	100.0%; Score 23; DB 12; Length 82;	Query Match	100.0%; Score 23; DB 2; Length 84;
Best Local Similarity	100.0%; Pred. No. 2.9e+02;	Best Local Similarity	100.0%; Pred. No. 3e+02;
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 DAHK 4	Qy	1 DAHK 4
Db	52 DAHK 55	Db	43 DAHK 46
RESULT 12		RESULT 14	
Q852V3	PRELIMINARY; PRT; 83 AA.	Q9JUN5	PRELIMINARY; PRT; 87 AA.
ID	Q852V3	AC	Q9JUN5
AC	Q852V3;	DT	01-OCT-2000 (TREMELrel. 15, Created)
DT	01-JUN-2003 (TREMELrel. 24, Last sequence update)	DT	01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT	01-JUN-2003 (TREMELrel. 24, Last annotation update)	DT	01-JUN-2003 (TREMELrel. 24, Last annotation update)
DE	Gp109.	DE	Hypothetical protein NMA1220.
GN	109.	GN	NMA1220.
OS	Mycobacteriophage Bx1.	OS	Neisseria meningitidis (serogroup A).
OC	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.	OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OX	NCBI_TaxID=205877;	OC	Neisseriaceae; Neisseria.
RN	[1]_TaxID=205877;	OX	NCBI_TaxID=65699;
RP	SEQUENCE FROM N.A.	RN	[1]
RX	MEDLINE=22592860; PubMed=12705866;	RP	SEQUENCE FROM N.A.
RA	Pedulla M.L., Ford M.E., Houtz J.M., Karthikeyan T., Wadsworth C.,	RC	STRAIN=22491 / Serogroup A / Serotype 4A;
RA	Lewis J.A., Jacobs-Sera D., Falbo J., Gross J., Panunzio N.R.,	RX	MEDLINE=20222556; PubMed=10761919;
RA	Brucker W., Kumar V., Kandasamy J., Keenan L., Bardarov S.,	RA	Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,
RA	Kriakov J., Lawrence J.G., Jacobs W.R. Jr., Hendrix R.W.,	RA	Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA	Hatfull G.F.;	RA	Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RT	"Origins of highly mosaic mycobacteriophage genomes.";	RA	Jagels K., Leather S., Moute S., Mungall K., Quail M.A.,
RL	Cell 113:171-182(2003).	RA	Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
DR	EMBL; AY129337; AAN16884.1; -	RA	Whitehead S., Spratt B.G., Barrall B.G.;
SQ	SEQUENCE 83 AA; 9426 MW; 32B2B3A17FBA92F8 CRC64;	RT	"Complete DNA sequence of a serogroup A strain of Neisseria
		RT	meningitidis Z2491.";
Query Match	100.0%; Score 23; DB 9; Length 83;	RL	Nature 404:502-506(2000).
Best Local Similarity	100.0%; Pred. No. 3e+02;	DR	EMBL; AL162755; CAB84480.1; -
Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	DR	PIR; C81890; C81890.
Qy	1 DAHK 4	KW	Hypothetical protein; Complete proteome.
Db	42 DAHK 45	SQ	SEQUENCE 87 AA; 9635 MW; 80058F6D4C9ADEA2 CRC64;
RESULT 13		Query Match	100.0%; Score 23; DB 16; Length 87;
Q9RG01	PRELIMINARY; PRT; 84 AA.	Best Local Similarity	100.0%; Pred. No. 3.1e+02;
ID	Q9RG01	Matches	4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AC	Q9RG01;	Qy	1 DAHK 4
DT	01-MAY-2000 (TREMELrel. 13, Created)	Db	46 DAHK 49
DT	01-MAY-2000 (TREMELrel. 13, Last sequence update)		
DT	01-OCT-2003 (TREMELrel. 25, Last annotation update)	RESULT 15	
DE	Fructose biphosphate aldolase (EC 4.1.2.13) (Fragment).	Q7VBB7	PRELIMINARY; PRT; 88 AA.
GN	FBA.	ID	Q7VBB7
OS	Mycoplasma capricolum subsp. capricolum.	AC	Q7VBB7;
OC	Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.	DT	01-OCT-2003 (TREMELrel. 25, Created)
OX	NCBI_TaxID=40479;	DT	01-OCT-2003 (TREMELrel. 25, Last sequence update)
RN	[1]	DT	01-OCT-2003 (TREMELrel. 25, Last annotation update)
RP	SEQUENCE FROM N.A.	DE	Putative heme iron utilization protein.
RX	STRAIN=7986;	GN	HUGZ OR PRO1180.
RX	MEDLINE=20193983; PubMed=10727835;	OS	Prochlorococcus marinus.
RA	Thiaucourt F., Lorenzen S., David A., Breard A.;	OS	Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococaceae;
RT	"Phylogeny of the Mycoplasma mycoides cluster as shown by sequencing	OC	Bacteria; Cyanobacteria; Prochlorococcus.
RT	of a putative membrane protein gene.";	OC	Prochlorococcus.
RL	Vet. Microbiol. 72:251-268(2000).	OX	NCBI_TaxID=1219;
DR	EMBL; AF162994; AAF15246.1; -	RN	[1]
GO	GO: 0004332; F-fructose-bisphosphate aldolase activity; IEA.		

RP SEQUENCE FROM N.A.  
 RC STRAIN=SARG / CCMP 1375 / SS120;  
 RX MEDLINE=22810154; PubMed=12917486;  
 RA Dufresne A., Salanoubat M., Partensky F., Artiguenave F., Axmann I.M.,  
 RA Barbe V., Duprat S., Galperin M.Y., Koonin E.V., Le Gall F.,  
 RA Makarova K.S., Ostrowski M., Oztras S., Robert C., Rogozin I.B.,  
 RA Scanlan D.J., Tandeau de Marsac N., Weissenbach J., Wincker P.,  
 RA Wolf Y.I., Hess W.R.;  
 RT "Genome sequence of the cyanobacterium Prochlorococcus marinus SS120,  
 RT a nearly minimal oxyphototrophic genome.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 100:10020-10025(2003).  
 DR EMBL; AB017164; AAQ00225.1; -.  
 KW Complete proteome.  
 SQ SEQUENCE 88 AA; 9821 MW; D922EEC9BF6AE2F7 CRC64;  
 Query Match 100.0%; Score 23; DB 16; Length 88;  
 Best Local Similarity 100.0%; Pred. NO. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAHK 4  
 Db 74 DAHK 77

Search completed: September 9, 2004, 23:47:56  
 Job time : 154 secs

Fri Sep 10 11:38:08 2004

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OM protein - protein search, using sw model

Run on: September 9, 2004, 23:32:32 ; Search time 125 Seconds

(without alignments)  
9.042 Million cell updates/sec

Title: US-10-076-071-1

Perfect score: 23

Sequence: 1 DAHX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 1000 summaries

Database : A\_Geneseq\_29Jan04.\*

1: Geneseq1980s.\*

2: Geneseq1990s.\*

3: Geneseq2000s.\*

4: Geneseq2001s.\*

5: Geneseq2002s.\*

6: Geneseq2003as.\*

7: Geneseq2003bs.\*

8: Geneseq2004s.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	4	3	Aay90711 Human alb
2	23	100.0	4	4	Aab74365 Reactive
3	23	100.0	4	4	Aab86898 Transport
4	23	100.0	4	5	Aae14799 Human ser
5	23	100.0	4	6	Abr39034 Acylated
6	23	100.0	4	6	Abp98620 Cu-chelat
7	23	100.0	4	6	Abp98473 Amino aci
8	23	100.0	4	6	Abp98473 Amino aci
9	23	100.0	5	6	Aaw23611 Prolactin
10	23	100.0	6	2	Aaw23634 Human pro
11	23	100.0	7	6	Abr39046 Acylated
12	23	100.0	8	3	Aay90712 Human alb
13	23	100.0	8	5	Abg70867 Fluoresce
14	23	100.0	9	4	Aae13134 Human alb
15	23	100.0	9	6	Abr39047 Acylated
16	23	100.0	10	4	Aag96326 Human com
17	23	100.0	10	4	Aag96328 Human com
18	23	100.0	11	6	Aar37401 Human ser
19	23	100.0	12	4	Aab74367 Reactive
20	23	100.0	12	4	Aab74370 Reactive
21	23	100.0	12	4	Aae14804 Human rea
22	23	100.0	12	5	Aae14801 Human rea
23	23	100.0	12	6	Abb99709 Biopolyme
24	23	100.0	12	6	Abb99709 Biopolyme
25	23	100.0	13	6	Abg75657 Congestiv

26	23	100.0	14	6	ABU08831	Abu08831 Serum alb
27	23	100.0	15	6	ABU08835	Abu08835 Serum alb
28	23	100.0	15	6	ABU09403	Renal fai
29	23	100.0	17	7	ADB61646	Abb61646 Human syn
30	23	100.0	20	3	AAB12462	Abb12462 Human alb
31	23	100.0	20	2	AAR80304	Invertase
32	23	100.0	24	2	AAO20109	Aao20109 24-mer pe
33	23	100.0	24	4	AAO20109	Aao20109 24-mer pe
34	23	100.0	24	4	AAE12402	Aae12402 Fusion pe
35	23	100.0	24	4	AAE13398	Aae13398 Fusion pe
36	23	100.0	24	4	AAE13398	Aae13398 Fusion pe
37	23	100.0	24	4	ABF79005	Abf79005 Human alb
38	23	100.0	24	5	AAU75219	Aau75219 SUC2 lead
39	23	100.0	24	5	ABG63320	Abg63320 S. cerevi
40	23	100.0	24	5	ABR55694	AbR55694 Invertase
41	23	100.0	24	7	ADD68005	Add68005 Yeast inv
42	23	100.0	26	2	AR37995	Aar37995 Aspergill
43	23	100.0	26	6	ABU08846	Abu08846 Serum alb
44	23	100.0	26	6	ABG75942	Abg75942 Human ser
45	23	100.0	28	6	ABU08847	Abu08847 Serum alb
46	23	100.0	28	6	ABU09223	Abu09223 Serum alb
47	23	100.0	32	4	ABR98752	AbR98752 Human sec
48	23	100.0	37	4	ABR98799	AbR98799 Human sec
49	23	100.0	37	4	ABH84272	Abh84272 Secondary
50	23	100.0	38	6	ABF78795	Abf78795 N. gonorr
51	23	100.0	41	4	ABR98822	AbR98822 Human sec
52	23	100.0	41	4	ABR98777	AbR98777 Human sec
53	23	100.0	41	4	ABR84292	AbR84292 Amino aci
54	23	100.0	42	3	ABR12839	AbR12839 Protein k
55	23	100.0	47	4	AAO09023	Aao09023 Human pol
56	23	100.0	53	4	ABM18531	Abm18531 Peptide #
57	23	100.0	53	4	ABM37566	Abm37566 Peptide #
58	23	100.0	53	4	ABM30988	Abm30988 Peptide #
59	23	100.0	53	4	ABM32307	Abm32307 Peptide #
60	23	100.0	53	4	ABM22861	Abm22861 Protein #
61	23	100.0	53	4	ABM70677	Abm70677 Human bon
62	23	100.0	53	4	ABM58223	Abm58223 Human bra
63	23	100.0	53	4	ABG52381	Abg52381 Human liv
64	23	100.0	53	4	ABM06099	Abm06099 Peptide #
65	23	100.0	53	5	ABG40382	Abg40382 Human pep
66	23	100.0	54	4	ABM14996	Abm14996 Human ner
67	23	100.0	55	3	ABG58879	Abg58879 Arabidops
68	23	100.0	57	5	AAE19578	Aae19578 Equine he
69	23	100.0	60	5	ABP10253	Abp10253 Human ORF
70	23	100.0	65	4	AAW91854	Aaw91854 Human imm
71	23	100.0	67	5	ABP10998	Abp10998 Human ORF
72	23	100.0	72	5	ABP35027	Abp35027 Human tra
73	23	100.0	73	5	ABP34960	Abp34960 Human ORF
74	23	100.0	87	6	ABP79101	Abp79101 N. gonorr
75	23	100.0	90	4	ABG03214	Abg03214 Novel hum
76	23	100.0	92	5	ABP41442	Abp41442 Human ova
77	23	100.0	94	4	ABM84542	Abm84542 Human ORF
78	23	100.0	96	5	ABP63825	Abp63825 Human ORF
79	23	100.0	97	4	AAO03583	Aao03583 Human pol
80	23	100.0	100	5	ABBS4788	Abbs4788 Lactococc
81	23	100.0	104	4	ABU03321	Abu03321 Human mus
82	23	100.0	104	4	ABU29873	Abu29873 Novel hum
83	23	100.0	104	6	ABU12615	Abu12615 Novel hum
84	23	100.0	104	6	ABU28386	Abu28386 Protein e
85	23	100.0	113	4	ABU44222	Abu44222 Human e
86	23	100.0	113	4	AAO11631	Aao11631 Human pol
87	23	100.0	114	3	AAU46378	Aau46378 Propionib
88	23	100.0	114	6	ABM42897	Abm42897 Human pol
89	23	100.0	116	4	AAO2642	Aao2642 Human nov
90	23	100.0	117	4	AAU16493	Aau16493 Human bre
91	23	100.0	117	4	AAU42255	Aau42255 Human rep
92	23	100.0	117	4	AAU94448	Aau94448 Human nov
93	23	100.0	117	6	AAU55562	Aau55562 Human nov
94	23	100.0	119	4	AAO11632	Aao11632 Human pol
95	23	100.0	120	4	ABG18807	Abg18807 Novel hum
96	23	100.0	121	4	AAU16064	Aau16064 Human nov
97	23	100.0	121	6	ABU55133	Abu55133 Human nov

99	23	100.0	123	4	AAO04424	Human pol	172	23	100.0	240	4	AAW94259	Human rep
100	23	100.0	124	4	AAO02630	Human pol	173	23	100.0	241	5	AAO16984	Alpha-MSH
101	23	100.0	124	4	AAO10348	Human pol	174	23	100.0	241	7	ABU10025	Alpha-MSH
102	23	100.0	125	3	ABE41211	Human ORF	175	23	100.0	242	5	AAO16985	Alpha-MSH
103	23	100.0	127	4	ABE63041	Drosophil	176	23	100.0	244	5	ABE65124	Drosophil
104	23	100.0	128	4	ABE63248	Drosophil	177	23	100.0	244	5	AAO16986	Alpha-MSH
105	23	100.0	132	4	AAO09589	Human pol	178	23	100.0	245	3	AAO16987	Alpha-MSH
106	23	100.0	133	1	AAO09589	Sequence	179	23	100.0	245	4	AAO16988	Alpha-MSH
107	23	100.0	133	1	AAO09589	Sequence	180	23	100.0	245	4	AAO16989	Alpha-MSH
108	23	100.0	134	3	AAO16390	Novel hum	181	23	100.0	245	5	AAO16990	Alpha-MSH
109	23	100.0	134	3	AAO16390	Novel hum	182	23	100.0	247	4	AAO16991	Alpha-MSH
110	23	100.0	137	4	AAO12088	Human pol	183	23	100.0	248	4	AAO16992	Alpha-MSH
111	23	100.0	138	5	ABP39993	Staphyloc	184	23	100.0	249	4	ABE69435	Drosophil
112	23	100.0	141	6	ABP79507	N. gonorr	185	23	100.0	252	5	ABU51265	Helicobac
113	23	100.0	142	4	AAO16390	Novel hum	186	23	100.0	257	5	ABU51001	Helicobac
114	23	100.0	144	6	AAO16390	Novel hum	187	23	100.0	259	5	ABU51009	Helicobac
115	23	100.0	145	4	ABG20922	Acinetoba	188	23	100.0	259	5	ABU51792	Helicobac
116	23	100.0	148	5	ABP42171	Novel hum	189	23	100.0	263	3	AAO16993	Alpha-MSH
117	23	100.0	149	6	ABE65278	Human ova	190	23	100.0	263	3	AAO16994	Alpha-MSH
118	23	100.0	153	4	AAO10773	Human pol	191	23	100.0	263	5	AAO16995	Alpha-MSH
119	23	100.0	155	4	AAO10773	Human pol	192	23	100.0	267	2	AAO16996	Alpha-MSH
120	23	100.0	159	5	ABE80777	C. glutami	193	23	100.0	268	5	AAO16997	Alpha-MSH
121	23	100.0	160	2	AAO10773	Human pol	194	23	100.0	268	7	ABU10026	Alpha-MSH
122	23	100.0	165	3	AAO10773	Human pol	195	23	100.0	270	5	ABU51448	Helicobac
123	23	100.0	166	3	AAO10773	Human pol	196	23	100.0	270	5	ABU52203	Helicobac
124	23	100.0	168	4	AAO10773	Human pol	197	23	100.0	271	3	AAO16998	Alpha-MSH
125	23	100.0	168	4	AAO10773	Human pol	198	23	100.0	271	3	AAO16999	Alpha-MSH
126	23	100.0	168	4	AAO10773	Human pol	199	23	100.0	271	3	AAO17000	Alpha-MSH
127	23	100.0	172	2	AAO10773	Human pol	200	23	100.0	271	3	AAO17001	Alpha-MSH
128	23	100.0	173	6	AAO10773	Human pol	201	23	100.0	271	3	AAO17002	Alpha-MSH
129	23	100.0	175	6	AAO10773	Human pol	202	23	100.0	271	3	AAO17003	Alpha-MSH
130	23	100.0	175	6	AAO10773	Human pol	203	23	100.0	271	3	AAO17004	Alpha-MSH
131	23	100.0	177	4	AAO10773	Human pol	204	23	100.0	271	3	AAO17005	Alpha-MSH
132	23	100.0	178	6	AAO10773	Human pol	205	23	100.0	271	3	AAO17006	Alpha-MSH
133	23	100.0	181	6	AAO10773	Human pol	206	23	100.0	271	3	AAO17007	Alpha-MSH
134	23	100.0	182	2	AAO10773	Human pol	207	23	100.0	271	3	AAO17008	Alpha-MSH
135	23	100.0	184	4	AAO10773	Human pol	208	23	100.0	271	3	AAO17009	Alpha-MSH
136	23	100.0	184	4	AAO10773	Human pol	209	23	100.0	271	3	AAO17010	Alpha-MSH
137	23	100.0	186	3	AAO10773	Human pol	210	23	100.0	271	3	AAO17011	Alpha-MSH
138	23	100.0	186	3	AAO10773	Human pol	211	23	100.0	271	3	AAO17012	Alpha-MSH
139	23	100.0	187	6	AAO10773	Human pol	212	23	100.0	271	3	AAO17013	Alpha-MSH
140	23	100.0	190	4	AAO10773	Human pol	213	23	100.0	271	3	AAO17014	Alpha-MSH
141	23	100.0	192	4	AAO10773	Human pol	214	23	100.0	271	3	AAO17015	Alpha-MSH
142	23	100.0	195	5	AAO10773	Human pol	215	23	100.0	271	3	AAO17016	Alpha-MSH
143	23	100.0	195	6	AAO10773	Human pol	216	23	100.0	271	3	AAO17017	Alpha-MSH
144	23	100.0	195	6	AAO10773	Human pol	217	23	100.0	271	3	AAO17018	Alpha-MSH
145	23	100.0	196	5	AAO10773	Human pol	218	23	100.0	271	3	AAO17019	Alpha-MSH
146	23	100.0	200	7	AAO10773	Human pol	219	23	100.0	271	3	AAO17020	Alpha-MSH
147	23	100.0	200	7	AAO10773	Human pol	220	23	100.0	271	3	AAO17021	Alpha-MSH
148	23	100.0	204	3	AAO10773	Human pol	221	23	100.0	271	3	AAO17022	Alpha-MSH
149	23	100.0	205	4	AAO10773	Human pol	222	23	100.0	271	3	AAO17023	Alpha-MSH
150	23	100.0	214	4	AAO10773	Human pol	223	23	100.0	271	3	AAO17024	Alpha-MSH
151	23	100.0	218	6	AAO10773	Human pol	224	23	100.0	271	3	AAO17025	Alpha-MSH
152	23	100.0	219	3	AAO10773	Human pol	225	23	100.0	271	3	AAO17026	Alpha-MSH
153	23	100.0	222	6	AAO10773	Human pol	226	23	100.0	271	3	AAO17027	Alpha-MSH
154	23	100.0	222	6	AAO10773	Human pol	227	23	100.0	271	3	AAO17028	Alpha-MSH
155	23	100.0	223	6	AAO10773	Human pol	228	23	100.0	271	3	AAO17029	Alpha-MSH
156	23	100.0	224	6	AAO10773	Human pol	229	23	100.0	271	3	AAO17030	Alpha-MSH
157	23	100.0	224	6	AAO10773	Human pol	230	23	100.0	271	3	AAO17031	Alpha-MSH
158	23	100.0	227	6	AAO10773	Human pol	231	23	100.0	271	3	AAO17032	Alpha-MSH
159	23	100.0	231	5	AAO10773	Human pol	232	23	100.0	271	3	AAO17033	Alpha-MSH
160	23	100.0	231	5	AAO10773	Human pol	233	23	100.0	271	3	AAO17034	Alpha-MSH
161	23	100.0	231	5	AAO10773	Human pol	234	23	100.0	271	3	AAO17035	Alpha-MSH
162	23	100.0	232	2	AAO10773	Human pol	235	23	100.0	271	3	AAO17036	Alpha-MSH
163	23	100.0	233	3	AAO10773	Human pol	236	23	100.0	271	3	AAO17037	Alpha-MSH
164	23	100.0	233	3	AAO10773	Human pol	237	23	100.0	271	3	AAO17038	Alpha-MSH
165	23	100.0	234	3	AAO10773	Human pol	238	23	100.0	271	3	AAO17039	Alpha-MSH
166	23	100.0	234	3	AAO10773	Human pol	239	23	100.0	271	3	AAO17040	Alpha-MSH
167	23	100.0	236	3	AAO10773	Human pol	240	23	100.0	271	3	AAO17041	Alpha-MSH
168	23	100.0	237	5	AAO10773	Human pol	241	23	100.0	271	3	AAO17042	Alpha-MSH
169	23	100.0	238	3	AAO10773	Human pol	242	23	100.0	271	3	AAO17043	Alpha-MSH
170	23	100.0	238	5	AAO10773	Human pol	243	23	100.0	271	3	AAO17044	Alpha-MSH
171	23	100.0	239	3	AAO10773	Human pol	244	23	100.0	271	3	AAO17045	Alpha-MSH

245	23	100.0	298	2	AAW95683	Aaw95683 Saccharom	318	23	100.0	357	6	ABU43319	Abu43319 Protein e
246	23	100.0	298	3	AAG23054	Aag23054 Arabidops	319	23	100.0	357	6	ABU42597	Abu42597 Protein e
247	23	100.0	298	4	ABG84912	Abg84912 Shrimp wh	320	23	100.0	357	6	ABU43180	Abu43180 Protein e
248	23	100.0	298	5	ABR52995	AbR52995 Protein s	321	23	100.0	357	6	ABU42750	Abu42750 Protein e
249	23	100.0	300	4	ABB67446	Abb67446 Drosophil	322	23	100.0	357	6	ABU42643	Abu42643 Protein e
250	23	100.0	300	6	ABU21414	Abu21414 Protein e	323	23	100.0	357	6	ABU42584	Abu42584 Protein e
251	23	100.0	300	6	ABU21414	Abu21414 Protein e	324	23	100.0	357	6	ABU42775	Abu42775 Protein e
252	23	100.0	303	2	AAU14178	Aau14178 Human ser	325	23	100.0	358	5	ABB93911	Abb93911 Herbicida
253	23	100.0	305	4	AAU34210	Aau34210 Staphyloc	326	23	100.0	360	4	AAU35785	Aau35785 Helicobac
254	23	100.0	306	3	AAU34210	Aau34210 Human pan	327	23	100.0	360	6	AAU30899	Abu30899 Protein e
255	23	100.0	308	6	AAW60946	Aaw60946 Streptoco	328	23	100.0	361	3	AAU11129	Aag11129 Arabidops
256	23	100.0	312	7	ADC96057	Adc96057 E. faeciu	329	23	100.0	361	3	AAG46095	Aag46095 Arabidops
257	23	100.0	316	4	AAU87354	Aau87354 Novel cen	330	23	100.0	364	4	ABB60565	Abb60565 Drosophil
258	23	100.0	318	4	AAU87354	Aau87354 Human pro	331	23	100.0	370	3	AAG51774	Aag51774 Arabidops
259	23	100.0	318	6	ABU35353	Abu35353 Protein e	332	23	100.0	370	3	AAG46143	Aag46143 Arabidops
260	23	100.0	319	5	AAU99517	Aau99517 Amino aci	333	23	100.0	370	3	AAG51777	Aag51777 Arabidops
261	23	100.0	324	4	AAG82790	Aag82790 S. epider	334	23	100.0	370	3	AAU17063	Aau17063 Human pol
262	23	100.0	325	3	AAG45840	Aag45840 Arabidops	335	23	100.0	373	1	AAU7635	Aau7635 Novel sig
263	23	100.0	325	6	ABP76742	Abp76742 N. gonorr	336	23	100.0	373	5	ABP39073	Abp39073 Staphyloc
264	23	100.0	325	6	ABP76742	Abp76742 N. gonorr	337	23	100.0	375	5	ABP39073	Abp39073 Staphyloc
265	23	100.0	326	4	AAU99732	Aau99732 Oryza sat	338	23	100.0	378	4	AAU17063	Aau17063 Human pol
266	23	100.0	326	4	AAU99732	Aau99732 Oryza sat	339	23	100.0	378	4	AAU17063	Aau17063 Human pol
267	23	100.0	328	3	AAU13757	Aau13757 Arabidops	340	23	100.0	378	4	AAU17063	Aau17063 Human pol
268	23	100.0	329	3	AAU23018	Aau23018 Arabidops	341	23	100.0	378	4	AAU17063	Aau17063 Human pol
269	23	100.0	329	3	AAU23018	Aau23018 Arabidops	342	23	100.0	378	4	AAU17063	Aau17063 Human pol
270	23	100.0	329	3	AAU23018	Aau23018 Arabidops	343	23	100.0	378	4	AAU17063	Aau17063 Human pol
271	23	100.0	329	3	AAU23018	Aau23018 Arabidops	344	23	100.0	378	4	AAU17063	Aau17063 Human pol
272	23	100.0	329	3	AAU23018	Aau23018 Arabidops	345	23	100.0	378	4	AAU17063	Aau17063 Human pol
273	23	100.0	329	3	AAU23018	Aau23018 Arabidops	346	23	100.0	378	4	AAU17063	Aau17063 Human pol
274	23	100.0	330	4	AAU37716	Aau37716 Streptoco	347	23	100.0	388	1	AAU90389	Aap90389 N-termina
275	23	100.0	330	4	AAU64345	Aau64345 Propionib	348	23	100.0	388	1	AAU90389	Aap90389 N-termina
276	23	100.0	330	6	ABU01586	Abu01586 S. pneumo	349	23	100.0	389	1	AAU90389	Aap90389 N-termina
277	23	100.0	330	6	ABU01586	Abu01586 S. pneumo	350	23	100.0	390	1	AAU90389	Aap90389 N-termina
278	23	100.0	330	6	ABU01586	Abu01586 S. pneumo	351	23	100.0	390	1	AAU90389	Aap90389 N-termina
279	23	100.0	330	6	ABU01586	Abu01586 S. pneumo	352	23	100.0	390	1	AAU90389	Aap90389 N-termina
280	23	100.0	336	5	ABP5202	Abp5202 Hypoxia-r	353	23	100.0	390	1	AAU90389	Aap90389 N-termina
281	23	100.0	336	5	ABP5202	Abp5202 Hypoxia-r	354	23	100.0	390	1	AAU90389	Aap90389 N-termina
282	23	100.0	337	4	AAU81531	Aau81531 S. epider	355	23	100.0	394	4	AAU81531	Aau81531 S. epider
283	23	100.0	337	4	AAU81531	Aau81531 S. epider	356	23	100.0	394	4	AAU81531	Aau81531 S. epider
284	23	100.0	337	4	AAU81531	Aau81531 S. epider	357	23	100.0	394	4	AAU81531	Aau81531 S. epider
285	23	100.0	337	4	AAU81531	Aau81531 S. epider	358	23	100.0	394	4	AAU81531	Aau81531 S. epider
286	23	100.0	337	4	AAU81531	Aau81531 S. epider	359	23	100.0	394	4	AAU81531	Aau81531 S. epider
287	23	100.0	337	4	AAU81531	Aau81531 S. epider	360	23	100.0	394	4	AAU81531	Aau81531 S. epider
288	23	100.0	337	4	AAU81531	Aau81531 S. epider	361	23	100.0	394	4	AAU81531	Aau81531 S. epider
289	23	100.0	337	4	AAU81531	Aau81531 S. epider	362	23	100.0	394	4	AAU81531	Aau81531 S. epider
290	23	100.0	337	4	AAU81531	Aau81531 S. epider	363	23	100.0	394	4	AAU81531	Aau81531 S. epider
291	23	100.0	337	4	AAU81531	Aau81531 S. epider	364	23	100.0	394	4	AAU81531	Aau81531 S. epider
292	23	100.0	337	4	AAU81531	Aau81531 S. epider	365	23	100.0	394	4	AAU81531	Aau81531 S. epider
293	23	100.0	337	4	AAU81531	Aau81531 S. epider	366	23	100.0	394	4	AAU81531	Aau81531 S. epider
294	23	100.0	337	4	AAU81531	Aau81531 S. epider	367	23	100.0	394	4	AAU81531	Aau81531 S. epider
295	23	100.0	337	4	AAU81531	Aau81531 S. epider	368	23	100.0	394	4	AAU81531	Aau81531 S. epider
296	23	100.0	337	4	AAU81531	Aau81531 S. epider	369	23	100.0	394	4	AAU81531	Aau81531 S. epider
297	23	100.0	337	4	AAU81531	Aau81531 S. epider	370	23	100.0	394	4	AAU81531	Aau81531 S. epider
298	23	100.0	337	4	AAU81531	Aau81531 S. epider	371	23	100.0	394	4	AAU81531	Aau81531 S. epider
299	23	100.0	337	4	AAU81531	Aau81531 S. epider	372	23	100.0	394	4	AAU81531	Aau81531 S. epider
300	23	100.0	337	4	AAU81531	Aau81531 S. epider	373	23	100.0	394	4	AAU81531	Aau81531 S. epider
301	23	100.0	337	4	AAU81531	Aau81531 S. epider	374	23	100.0	394	4	AAU81531	Aau81531 S. epider
302	23	100.0	337	4	AAU81531	Aau81531 S. epider	375	23	100.0	394	4	AAU81531	Aau81531 S. epider
303	23	100.0	337	4	AAU81531	Aau81531 S. epider	376	23	100.0	394	4	AAU81531	Aau81531 S. epider
304	23	100.0	337	4	AAU81531	Aau81531 S. epider	377	23	100.0	394	4	AAU81531	Aau81531 S. epider
305	23	100.0	337	4	AAU81531	Aau81531 S. epider	378	23	100.0	394	4	AAU81531	Aau81531 S. epider
306	23	100.0	337	4	AAU81531	Aau81531 S. epider	379	23	100.0	394	4	AAU81531	Aau81531 S. epider
307	23	100.0	337	4	AAU81531	Aau81531 S. epider	380	23	100.0	394	4	AAU81531	Aau81531 S. epider
308	23	100.0	337	4	AAU81531	Aau81531 S. epider	381	23	100.0	394	4	AAU81531	Aau81531 S. epider
309	23	100.0	337	4	AAU81531	Aau81531 S. epider	382	23	100.0	394	4	AAU81531	Aau81531 S. epider
310	23	100.0	337	4	AAU81531	Aau81531 S. epider	383	23	100.0	394	4	AAU81531	Aau81531 S. epider
311	23	100.0	337	4	AAU81531	Aau81531 S. epider	384	23	100.0	394	4	AAU81531	Aau81531 S. epider
312	23	100.0	337	4	AAU81531	Aau81531 S. epider	385	23	100.0	394	4	AAU81531	Aau81531 S. epider
313	23	100.0	337	4	AAU81531	Aau81531 S. epider	386	23	100.0	394	4	AAU81531	Aau81531 S. epider
314	23	100.0	337	4	AAU81531	Aau81531 S. epider	387	23	100.0	394	4	AAU81531	Aau81531 S. epider
315	23	100.0	337	4	AAU81531	Aau81531 S. epider	388	23	100.0	394	4	AAU81531	Aau81531 S. epider
316	23	100.0	337	4	AAU81531	Aau81531 S. epider	389	23	100.0	394	4	AAU81531	Aau81531 S. epider
317	23	100.0	337	4	AAU81531	Aau81531 S. epider	390	23	100.0	394	4	AAU81531	Aau81531 S. epider

391	23	100.0	461	6	ABM69616	Abm69616 Phototrab	464	23	100.0	585	2	AAR05318	Aar05318 Human ser
392	23	100.0	461	6	ABM70151	Abm70151 Phototrab	465	23	100.0	585	2	AAR08457	Aar08457 Human ser
393	23	100.0	466	3	AAG46126	Aag46126 Arabidops	466	23	100.0	585	2	AAR26207	Aar26207 Human ser
394	23	100.0	466	3	AAG51772	Aag51772 Arabidops	467	23	100.0	585	2	AAR26362	Aar26362 Synthetic
395	23	100.0	467	5	ABP69216	Abp69216 Human pol	468	23	100.0	585	2	AAR20029	Aar20029 Human ser
396	23	100.0	467	5	ABP9338	Abp9338 Herbicida	469	23	100.0	585	2	AAR80301	Aar80301 Human ser
397	23	100.0	469	2	AAR22359	Aar22359 Histidino	470	23	100.0	585	2	AAR20111	Aar20111 HSA prote
398	23	100.0	469	2	AAG90154	Aag90154 C glutami	471	23	100.0	585	2	AAR59841	Aar59841 Mature pr
399	23	100.0	469	4	AAB73380	Aab73380 Moraxella	472	23	100.0	585	3	AAH84873	Aah84873 Amino aci
400	23	100.0	469	4	AAB83184	Aab83184 Corynebac	473	23	100.0	585	4	AAH83946	Aah83946 Yeast cod
401	23	100.0	470	5	AAE19560	Aae19560 Equine he	474	23	100.0	585	4	AAH52567	Aah52567 Mature hu
402	23	100.0	482	7	ABM78972	Abm78972 Arabidops	475	23	100.0	585	4	AAE12417	Aae12417 Human alb
403	23	100.0	484	2	AAW55700	Aaw55700 H. pylori	476	23	100.0	585	4	AAE12403	Aae12403 Human alb
404	23	100.0	484	2	AAW55700	Aaw55700 H. pylori	477	23	100.0	585	4	AAE13129	Aae13129 Human alb
405	23	100.0	484	2	AAW55700	Aaw55700 H. pylori	478	23	100.0	585	4	AAE13135	Aae13135 Human alb
406	23	100.0	484	2	AAW55700	Aaw55700 H. pylori	479	23	100.0	585	4	AAE13311	Aae13311 Human alb
407	23	100.0	484	2	AAW55700	Aaw55700 H. pylori	480	23	100.0	585	4	AAE13399	Aae13399 Human alb
408	23	100.0	485	4	AAH48945	Aah48945 Human ang	481	23	100.0	585	4	ABH79006	Aab79006 Human mat
409	23	100.0	485	4	AAH48945	Aah48945 Human ang	482	23	100.0	585	4	AAE08578	Aae08578 Human ser
410	23	100.0	485	4	AAH48945	Aah48945 Human ang	483	23	100.0	585	5	AAU75220	Aau75220 Mature fo
411	23	100.0	485	4	AAH48945	Aah48945 Human ang	484	23	100.0	585	5	ABU00986	Abu00986 B lymphoc
412	23	100.0	485	4	AAH48945	Aah48945 Human ang	485	23	100.0	585	5	ABG63321	Abg63321 Human ser
413	23	100.0	485	4	AAH48945	Aah48945 Human ang	486	23	100.0	585	5	ABG33847	Abg33847 Human B L
414	23	100.0	485	4	AAH48945	Aah48945 Human ang	487	23	100.0	585	5	ABG71291	Abg71291 Glycosyla
415	23	100.0	485	4	AAH48945	Aah48945 Human ang	488	23	100.0	585	6	ABG72380	Abg72380 Mature hu
416	23	100.0	488	5	ABP38075	Abp38075 Staphyloc	489	23	100.0	585	6	ABR55695	AbR55695 Human alb
417	23	100.0	491	6	ABM69741	Abm69741 Phototrab	490	23	100.0	585	6	AAE30936	Aae30936 Human alb
418	23	100.0	493	4	ABH71469	Abh71469 Drosophil	491	23	100.0	585	6	ABP98782	Abp98782 Mature hu
419	23	100.0	494	4	ABH68783	Abh68783 Drosophil	492	23	100.0	585	7	ABR42606	AbR42606 Human ser
420	23	100.0	494	4	ABH71945	Abh71945 Drosophil	493	23	100.0	585	7	ADC16767	Adc16767 Human ser
421	23	100.0	494	6	ABO52949	AbO52949 Human spl	494	23	100.0	585	7	ADC16794	Adc16794 Mutant hu
422	23	100.0	496	5	AAO26369	Aao26369 EHD1 deri	495	23	100.0	585	7	ADC16795	Adc16795 Mutant hu
423	23	100.0	500	6	AAO26369	Aao26369 EHD1 deri	496	23	100.0	585	7	ADD06469	Add06469 Human ser
424	23	100.0	500	7	ADD32019	Add32019 Heterolog	497	23	100.0	585	7	ADD32014	Add32014 Heterolog
425	23	100.0	501	6	ABM68457	Abm68457 Phototrab	498	23	100.0	586	1	AAE60072	Aae60072 Mature fo
426	23	100.0	505	2	AAW61027	Aaw61027 Murine gu	499	23	100.0	586	1	AAE60839	Aae60839 Sequence
427	23	100.0	507	4	ABH71378	Abh71378 Drosophil	500	23	100.0	586	1	AAE60839	Aae60839 Sequence
428	23	100.0	507	4	ABH71378	Abh71378 Drosophil	501	23	100.0	586	1	AAE60839	Aae60839 Sequence
429	23	100.0	507	4	ABH71378	Abh71378 Drosophil	502	23	100.0	586	1	AAE60839	Aae60839 Sequence
430	23	100.0	507	4	ABH71378	Abh71378 Drosophil	503	23	100.0	586	1	AAE60839	Aae60839 Sequence
431	23	100.0	508	2	AAW64772	Aaw64772 Serine th	504	23	100.0	586	1	AAE60839	Aae60839 Sequence
432	23	100.0	508	4	ABH60795	Abh60795 Drosophil	505	23	100.0	586	1	AAE60839	Aae60839 Sequence
433	23	100.0	508	4	ABH72676	Abh72676 Drosophil	506	23	100.0	586	1	AAE60839	Aae60839 Sequence
434	23	100.0	508	4	ABH72680	Abh72680 Drosophil	507	23	100.0	586	1	AAE60839	Aae60839 Sequence
435	23	100.0	510	2	AAH35221	Aah35221 Chlamydia	508	23	100.0	586	1	AAE60839	Aae60839 Sequence
436	23	100.0	510	6	ABU30442	Abu30442 Protein e	509	23	100.0	586	1	AAE60839	Aae60839 Sequence
437	23	100.0	517	4	ABH70723	Abh70723 Drosophil	510	23	100.0	586	1	AAE60839	Aae60839 Sequence
438	23	100.0	520	3	AAH36491	Aah36491 Human TUL	511	23	100.0	586	1	AAE60839	Aae60839 Sequence
439	23	100.0	520	3	AAH36491	Aah36491 Human TUL	512	23	100.0	586	1	AAE60839	Aae60839 Sequence
440	23	100.0	520	3	AAH36491	Aah36491 Human TUL	513	23	100.0	586	1	AAE60839	Aae60839 Sequence
441	23	100.0	521	6	ABH4652	Abh4652 Novel hum	514	23	100.0	586	1	AAE60839	Aae60839 Sequence
442	23	100.0	521	6	ABH4652	Abh4652 Novel hum	515	23	100.0	586	1	AAE60839	Aae60839 Sequence
443	23	100.0	521	6	ABH4652	Abh4652 Novel hum	516	23	100.0	586	1	AAE60839	Aae60839 Sequence
444	23	100.0	521	6	ABH4652	Abh4652 Novel hum	517	23	100.0	586	1	AAE60839	Aae60839 Sequence
445	23	100.0	521	6	ABH4652	Abh4652 Novel hum	518	23	100.0	586	1	AAE60839	Aae60839 Sequence
446	23	100.0	521	6	ABH4652	Abh4652 Novel hum	519	23	100.0	586	1	AAE60839	Aae60839 Sequence
447	23	100.0	521	6	ABH4652	Abh4652 Novel hum	520	23	100.0	586	1	AAE60839	Aae60839 Sequence
448	23	100.0	521	6	ABH4652	Abh4652 Novel hum	521	23	100.0	586	1	AAE60839	Aae60839 Sequence
449	23	100.0	521	6	ABH4652	Abh4652 Novel hum	522	23	100.0	586	1	AAE60839	Aae60839 Sequence
450	23	100.0	521	6	ABH4652	Abh4652 Novel hum	523	23	100.0	586	1	AAE60839	Aae60839 Sequence
451	23	100.0	521	6	ABH4652	Abh4652 Novel hum	524	23	100.0	586	1	AAE60839	Aae60839 Sequence
452	23	100.0	521	6	ABH4652	Abh4652 Novel hum	525	23	100.0	586	1	AAE60839	Aae60839 Sequence
453	23	100.0	521	6	ABH4652	Abh4652 Novel hum	526	23	100.0	586	1	AAE60839	Aae60839 Sequence
454	23	100.0	521	6	ABH4652	Abh4652 Novel hum	527	23	100.0	586	1	AAE60839	Aae60839 Sequence
455	23	100.0	521	6	ABH4652	Abh4652 Novel hum	528	23	100.0	586	1	AAE60839	Aae60839 Sequence
456	23	100.0	521	6	ABH4652	Abh4652 Novel hum	529	23	100.0	586	1	AAE60839	Aae60839 Sequence
457	23	100.0	521	6	ABH4652	Abh4652 Novel hum	530	23	100.0	586	1	AAE60839	Aae60839 Sequence
458	23	100.0	521	6	ABH4652	Abh4652 Novel hum	531	23	100.0	586	1	AAE60839	Aae60839 Sequence
459	23	100.0	521	6	ABH4652	Abh4652 Novel hum	532	23	100.0	586	1	AAE60839	Aae60839 Sequence
460	23	100.0	521	6	ABH4652	Abh4652 Novel hum	533	23	100.0	586	1	AAE60839	Aae60839 Sequence
461	23	100.0	521	6	ABH4652	Abh4652 Novel hum	534	23	100.0	586	1	AAE60839	Aae60839 Sequence
462	23	100.0	521	6	ABH4652	Abh4652 Novel hum	535	23	100.0	586	1	AAE60839	Aae60839 Sequence
463	23	100.0	521	6	ABH4652	Abh4652 Novel hum	536	23	100.0	586	1	AAE60839	Aae60839 Sequence



537	23	100.0	618	7	ADD71142	Adg71142 Human int	610	23	100.0	750	4	AAU29878	Aau29878 Novel hum
538	23	100.0	620	6	ABP98783	Abp98783 Full leng	611	23	100.0	750	4	AAU29881	Aau29881 Novel hum
539	23	100.0	621	2	AAR37870	Aar37870 Soluble K	612	23	100.0	750	6	ABU47656	Abu47656 Protein e
540	23	100.0	622	2	AAR20469	Aar20469 Soluble Y	613	23	100.0	753	4	AAR34588	Aar34588 E. coli c
541	23	100.0	623	5	ABB77434	Abb77434 Human tum	614	23	100.0	753	6	ABU14954	Abu14954 Protein e
542	23	100.0	624	5	ABB55583	Abb55583 Lactococc	615	23	100.0	754	2	AAR92149	Aar92149 HSA:Fc ga
543	23	100.0	624	6	AAR30919	Aar30919 Human ser	616	23	100.0	765	4	ABG28515	Abg28515 Novel hum
544	23	100.0	625	4	ABB58986	Abb58986 Drosophil	617	23	100.0	766	4	ABU53068	Abu53068 Transport
545	23	100.0	630	4	ABR31102	AbR31102 Human pro	618	23	100.0	779	6	ABR83434	AbR83434 HSA-TIMP2
546	23	100.0	631	2	AAR96230	Aar96230 Human ser	619	23	100.0	783	2	AAR39473	Aar39473 Prepro-HS
547	23	100.0	631	4	ABB65808	Abb65808 Drosophil	620	23	100.0	787	2	AAR39477	Aar39477 G-CSF-(G1
548	23	100.0	631	6	AAR30917	Aar30917 Val8-GLP-	621	23	100.0	789	4	AAU29880	Aau29880 Novel hum
549	23	100.0	632	2	AAR96231	Aar96231 Human ser	622	23	100.0	789	4	ADG63953	Adg63953 Rat Prote
550	23	100.0	635	4	ABR71475	AbR71475 Drosophil	623	23	100.0	791	3	AAY75756	Aay75756 Neisseria
551	23	100.0	639	6	ABU20668	Abu20668 Protein e	624	23	100.0	791	6	ABP79242	Abp79242 N. gonorr
552	23	100.0	640	6	AAE30920	Aae30920 Extensin-4	625	23	100.0	792	3	AAU75754	Aau75754 Neisseria
553	23	100.0	640	3	AAE30918	Aae30918 Gly8-Glu2	626	23	100.0	796	5	AAG66076	Aag66076 N. mening
554	23	100.0	641	3	AAY75755	Aay75755 Neisseria	627	23	100.0	801	6	ABM70487	Abm70487 Photorhab
555	23	100.0	651	7	ADD06597	Add06597 Human Ckb	628	23	100.0	802	4	AAU95231	Aau95231 Human pro
556	23	100.0	652	7	ADD06563	Add06563 Human Ckb	629	23	100.0	810	4	AAU81232	Aau81232 Mycobacte
557	23	100.0	652	7	ADD06596	Add06596 Human Ckb	630	23	100.0	814	1	AAU90681	Aau90681 KEX2 endo
558	23	100.0	652	7	ADD06596	Add06596 Human Ckb	631	23	100.0	814	1	AAU25685	Aau25685 KEX2 prot
559	23	100.0	653	7	ADD06595	Add06595 Human Ckb	632	23	100.0	815	6	ADA32997	Ada32997 Acinetoba
560	23	100.0	656	7	ADD06594	Add06594 Human Ckb	633	23	100.0	823	4	ABG25584	Abg25584 Novel hum
561	23	100.0	656	7	ADD06594	Add06594 Human Ckb	634	23	100.0	825	6	ABR52748	AbR52748 Protein s
562	23	100.0	659	7	ADCL6791	Adcl6791 Chimeric	635	23	100.0	830	6	ABM68441	Abm68441 Photorhab
563	23	100.0	659	7	ADCL6793	Adcl6793 Chimeric	636	23	100.0	830	6	ABR52748	AbR52748 Protein s
564	23	100.0	660	7	ADD06557	Add06557 Human Ckb	637	23	100.0	835	2	AAU39472	Aau39472 HSA-vWF(4
565	23	100.0	660	7	ADD06554	Add06554 Human Ckb	638	23	100.0	853	2	AAU39472	Aau39472 HSA-vWF(4
566	23	100.0	662	7	ADCL6789	Adcl6789 Chimeric	639	23	100.0	865	6	ABU14972	Abu14972 Protein e
567	23	100.0	662	7	ADCL6787	Adcl6787 Chimeric	640	23	100.0	865	6	ABU14972	Abu14972 Protein e
568	23	100.0	668	4	AAU94411	Aau94411 Human pro	641	23	100.0	868	4	ABU26316	Abu26316 Protein e
569	23	100.0	668	5	ABB54996	Abb54996 Lactococ	642	23	100.0	871	6	ABU26316	Abu26316 Protein e
570	23	100.0	668	6	ABU44992	Abu44992 Protein e	643	23	100.0	876	6	ABU49402	Abu49402 Protein e
571	23	100.0	668	7	ADD06566	Add06566 Human Ckb	644	23	100.0	879	4	AAU29879	Aau29879 Novel hum
572	23	100.0	670	3	AAU36543	Aau36543 Recombina	645	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
573	23	100.0	670	3	AAU36550	Aau36550 Recombina	646	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
574	23	100.0	671	5	ABF51430	Abf51430 Human MDD	647	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
575	23	100.0	672	7	ABR42610	AbR42610 Fusion pr	648	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
576	23	100.0	674	7	ABR42610	AbR42610 Fusion pr	649	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
577	23	100.0	676	4	ABR58042	AbR58042 Drosophil	650	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
578	23	100.0	676	7	ADD06591	Add06591 Human Ckb	651	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
579	23	100.0	676	7	ADD06591	Add06591 Human Ckb	652	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
580	23	100.0	676	7	ADD06568	Add06568 Human Ckb	653	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
581	23	100.0	676	7	ADD06559	Add06559 Human Ckb	654	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
582	23	100.0	676	7	ADD06552	Add06552 Human Ckb	655	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
583	23	100.0	677	7	ADD06593	Add06593 Human Ckb	656	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
584	23	100.0	680	7	ADD06589	Add06589 Human Ckb	657	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
585	23	100.0	684	4	AAU33090	Aau33090 Novel hum	658	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
586	23	100.0	684	7	ADD06556	Add06556 Human Ckb	659	23	100.0	883	2	AAU69627	Aau69627 Bacteriop
587	23	100.0	687	7	ABR42612	AbR42612 Fusion pr	660	23	100.0	898	4	ABR53073	AbR53073 Intracell
588	23	100.0	688	7	ABR42613	AbR42613 Fusion pr	661	23	100.0	907	4	ABR53073	AbR53073 Intracell
589	23	100.0	689	7	ABR42608	AbR42608 Fusion pr	662	23	100.0	915	4	ABR70955	AbR70955 Drosophil
590	23	100.0	692	7	ADD06565	Add06565 Human Ckb	663	23	100.0	941	4	ABU53072	Abu53072 Intracell
591	23	100.0	696	4	ABB61188	Abb61188 Drosophil	664	23	100.0	949	5	ABP69203	Abp69203 Human pol
592	23	100.0	701	4	AAU94767	Aau94767 Human pro	665	23	100.0	949	5	ABP69357	Abp69357 Human pol
593	23	100.0	702	4	AAU34524	Aau34524 E. coli c	666	23	100.0	949	6	ABU03470	Abu03470 Angiogene
594	23	100.0	702	4	AAU34524	Aau34524 E. coli c	667	23	100.0	949	6	ABU03470	Abu03470 Angiogene
595	23	100.0	703	5	ABR93466	AbR93466 Herbicida	668	23	100.0	949	6	ABU03470	Abu03470 Angiogene
596	23	100.0	710	2	AAW80995	Aaw80995 Human gua	669	23	100.0	951	4	ABU53072	Abu53072 Intracell
597	23	100.0	711	6	AAU39585	Aau39585 Protein e	670	23	100.0	951	4	ABU53072	Abu53072 Intracell
598	23	100.0	712	2	AAU39585	Aau39585 Protein e	671	23	100.0	955	6	ADA55002	Ada55002 Human pro
599	23	100.0	714	5	ABG39810	Abg39810 Transcrip	672	23	100.0	961	4	ABU53077	Abu53077 Intracell
600	23	100.0	715	5	AAU71801	Aau71801 Zinc fing	673	23	100.0	961	4	ABU53077	Abu53077 Intracell
601	23	100.0	718	2	AAU12560	Aau12560 HSA-IL-2	674	23	100.0	978	4	ABU53077	Abu53077 Intracell
602	23	100.0	734	6	AAU725384	Aau725384 Aspergill	675	23	100.0	978	5	ABG32803	Abg32803 Human Ige
603	23	100.0	736	5	AAU49042	Aau49042 Acaryochl	676	23	100.0	984	4	AAU33272	Aau33272 Novel hum
604	23	100.0	738	4	ABB58451	Abb58451 Drosophil	677	23	100.0	988	4	AAU33272	Aau33272 Novel hum
605	23	100.0	738	4	AAU38924	Aau38924 Drosophil	678	23	100.0	1013	6	ABJ25984	Abj25984 Aspergill
606	23	100.0	738	7	ADC35754	Adc35754 Drosophil	679	23	100.0	1021	5	ABP73550	Abp73550 Candida a
607	23	100.0	743	5	ABP35672	Abp35672 Fungal ZB	680	23	100.0	1025	2	AAU43596	Aau43596 Amino aci
608	23	100.0	748	4	ABB64114	Abb64114 Drosophil	681	23	100.0	1025	2	AAU43596	Aau43596 Amino aci
609	23	100.0	749	6	ABU27823	Abu27823 Protein e	682	23	100.0	1025	6	AAU26664	Aau26664 Human IRA
	23	100.0	750	4	AAU38392	Aau38392 Salmonell							

683	23	100.0	1025	6	AAG79732	Agg79732 Rat IRAP.	756	20	87.0	7	7	ABR62810	AbR62810 9-G5 pept
684	23	100.0	1025	7	ADD48134	Add48134 Rat Prote	757	20	87.0	8	8	AAU03791	Aau03791 P21-activ
685	23	100.0	1026	7	AAR94511	Aar94511 GTVap (lo	758	20	87.0	8	6	ADBL17035	Adbl17035 Peptide s
686	23	100.0	1026	2	AAy43597	Aay43597 Amino aci	759	20	87.0	9	7	ADC44572	Adc44572 Endotheli
687	23	100.0	1043	6	ARU22178	ArU22178 Protein e	760	20	87.0	11	2	AAW23623	Aaw23623 Rat prola
688	23	100.0	1070	7	ADC94089	Adc94089 E. faeciu	761	20	87.0	11	2	AAW23623	Aaw23623 Rat prola
689	23	100.0	1090	6	ABP98840	Abp98840 Human str	762	20	87.0	11	2	AAW23623	Aaw23623 Rat prola
690	23	100.0	1094	4	ABG28526	Abg28526 Novel hum	763	20	87.0	13	3	AB229695	Ab229695 Mouse apo
691	23	100.0	1098	6	ABO07120	AbO07120 Novel hum	764	20	87.0	13	3	AAO19557	Aao19557 Modified
692	23	100.0	1109	5	ABR91480	AbR91480 Herbicida	765	20	87.0	15	2	AAO19557	Aao19557 Modified
693	23	100.0	1134	6	ABR53120	AbR53120 Protein s	766	20	87.0	15	2	AAO19557	Aao19557 Modified
694	23	100.0	1152	6	ABM67058	Abm67058 Phototrab	767	20	87.0	15	2	AAO19557	Aao19557 Modified
695	23	100.0	1166	6	ABU40581	Abu40581 Protein e	768	20	87.0	15	2	AAO19557	Aao19557 Modified
696	23	100.0	1177	1	AAp70187	Aap70187 Plasmid p	769	20	87.0	19	2	AAW23616	Aaw23616 ProLactin
697	23	100.0	1180	4	ABB60588	Abb60588 Drosophil	770	20	87.0	20	2	AAW23616	Aaw23616 ProLactin
698	23	100.0	1184	7	ADD06553	AdD06553 Human Ckb	771	20	87.0	20	2	AAW23616	Aaw23616 ProLactin
699	23	100.0	1189	2	AAR08399	Aar08399 Human Ser	772	20	87.0	22	4	AAW23616	Aaw23616 ProLactin
700	23	100.0	1190	4	ABB60516	Abb60516 Drosophil	773	20	87.0	22	4	AAW23616	Aaw23616 ProLactin
701	23	100.0	1225	4	AAU18529	Aau18529 Human cyt	774	20	87.0	25	4	AAW23616	Aaw23616 ProLactin
702	23	100.0	1247	6	ABJ19352	Abj19352 NOXK rela	775	20	87.0	25	4	AAW23616	Aaw23616 ProLactin
703	23	100.0	1248	4	ABB61571	Abb61571 Drosophil	776	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
704	23	100.0	1257	2	AAy06427	Aay06427 Mouse cir	777	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
705	23	100.0	1273	4	AAW41011	Aaw41011 Human pol	778	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
706	23	100.0	1279	4	AAW83047	Aaw83047 S. epider	779	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
707	23	100.0	1280	6	ABU00615	Abu00615 S. pneumo	780	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
708	23	100.0	1327	5	ABW97286	Abw97286 Novel hum	781	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
709	23	100.0	1381	2	AAR08032	Aar08032 Human Ser	782	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
710	23	100.0	1443	6	ABG74688	Abg74688 Human CGD	783	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
711	23	100.0	1493	4	AAW39225	Aaw39225 Human pol	784	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
712	23	100.0	1526	4	ABB63939	Abb63939 Drosophil	785	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
713	23	100.0	1551	4	ABB64459	Abb64459 Drosophil	786	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
714	23	100.0	1565	4	ABG18593	Abg18593 Novel hum	787	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
715	23	100.0	1604	4	AAW47327	Aaw47327 FCTR4. 8/	788	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
716	23	100.0	1775	4	ABW64008	Abw64008 Drosophil	789	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
717	23	100.0	1798	4	ABW1695	Abw1695 Drosophil	790	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
718	23	100.0	1917	6	ABW99738	Abw99738 Polypepti	791	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
719	23	100.0	1967	6	AAE35342	Aae35342 Human col	792	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
720	23	100.0	1967	6	AAE35342	Aae35342 Human col	793	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
721	23	100.0	2001	6	ABU70405	Abu70405 Human chr	794	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
722	23	100.0	2051	6	AAO19619	Aao19619 Human adi	795	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
723	23	100.0	2061	4	ABW66938	Abw66938 Drosophil	796	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
724	23	100.0	2215	5	ABW85015	Abw85015 Pain regu	797	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
725	23	100.0	2215	5	ABW85015	Abw85015 Pain regu	798	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
726	23	100.0	2228	7	ABR61599	AbR61599 Human gol	799	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
727	23	100.0	2230	6	ABU07445	Abu07445 Protein d	800	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
728	23	100.0	2230	6	ABU07445	Abu07445 Protein d	801	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
729	23	100.0	2250	7	ABR61601	AbR61601 Human gol	802	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
730	23	100.0	2250	7	ABR61601	AbR61601 Human gol	803	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
731	23	100.0	2370	4	ABW62050	Abw62050 Drosophil	804	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
732	23	100.0	2457	6	ABU21930	Abu21930 Protein e	805	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
733	23	100.0	2559	2	AAW11012	Aaw11012 Amino aci	806	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
734	23	100.0	2559	2	AAW11012	Aaw11012 Amino aci	807	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
735	23	100.0	2670	4	AAW88126	Aaw88126 Drosophil	808	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
736	23	100.0	2670	4	AAW88126	Aaw88126 Drosophil	809	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
737	23	100.0	3079	2	AAW59926	Aaw59926 GAP prote	810	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
738	23	100.0	3084	2	AAW50891	Aaw50891 Mouse lam	811	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
739	23	100.0	3084	2	AAW50891	Aaw50891 Mouse lam	812	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
740	23	100.0	3111	4	ABW60327	Abw60327 Drosophil	813	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
741	23	100.0	3269	6	ABP54436	Abp54436 Papaya le	814	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
742	23	100.0	3542	4	ABW62142	Abw62142 P. falcip	815	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
743	23	100.0	3673	6	ABW68688	Abw68688 Phototrab	816	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
744	23	100.0	3692	6	ABU43311	Abu43311 Protein e	817	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
745	23	100.0	3696	5	ABP40235	Abp40235 Staphyloc	818	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
746	23	100.0	4820	4	ABW58592	Abw58592 Drosophil	819	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
747	23	100.0	4861	5	AAU84280	Aau84280 Human end	820	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
748	23	100.0	4861	5	AAU84280	Aau84280 Human end	821	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
749	23	100.0	4861	7	ADC35083	AdC35083 HERR1 pro	822	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
750	23	100.0	5373	4	AAU14603	Aau14603 Novel bon	823	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
751	23	100.0	5447	4	AAU14697	Aau14697 Novel bon	824	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
752	23	100.0	5447	4	AAU14697	Aau14697 Novel bon	825	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
753	23	100.0	5447	4	AAU14697	Aau14697 Novel bon	826	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
754	23	100.0	5447	4	AAU14697	Aau14697 Novel bon	827	20	87.0	31	4	AAW23616	Aaw23616 ProLactin
755	23	100.0	5447	4	AAU14697	Aau14697 Novel bon	828	20	87.0	31	4	AAW23616	Aaw23616 ProLactin

829 20 87.0 59 4 AAU48607 Propionib  
830 20 87.0 59 6 ABM45126 Propionib  
831 20 87.0 60 4 AAU43739 Propionib  
832 20 87.0 60 5 ABP07135 Human ORF  
833 20 87.0 60 6 ABM40258 Propionib  
834 20 87.0 62 4 AAU44216 Propionib  
835 20 87.0 62 4 AAU50652 Propionib  
836 20 87.0 62 4 AAU63496 Propionib  
837 20 87.0 62 6 ABM60015 Propionib  
838 20 87.0 62 6 ABM40735 Propionib  
839 20 87.0 62 6 ABM47171 Propionib  
840 20 87.0 63 4 AAU52464 Propionib  
841 20 87.0 63 6 ABM48983 Propionib  
842 20 87.0 64 4 AAG90481 C glutami  
843 20 87.0 66 5 ABP04669 Human ORF  
844 20 87.0 67 4 AAU39252 Propionib  
845 20 87.0 67 6 ABM35771 Propionib  
846 20 87.0 68 4 ABM92836 Human dig  
847 20 87.0 68 4 AAU44715 Propionib  
848 20 87.0 68 5 ABP06151 Human ORF  
849 20 87.0 68 6 ABM41234 Propionib  
850 20 87.0 69 4 ABG30198 Novel hum  
851 20 87.0 70 4 AAU60967 Propionib  
852 20 87.0 70 6 ABM57486 Propionib  
853 20 87.0 71 2 AAU60082 Human end  
854 20 87.0 71 3 AAG40993 Zea mays  
855 20 87.0 71 4 AAU67693 Propionib  
856 20 87.0 71 4 AAU44404 Propionib  
857 20 87.0 71 4 ABG15549 Novel hum  
858 20 87.0 71 6 ABM40923 Propionib  
859 20 87.0 71 6 ABM64212 Propionib  
860 20 87.0 73 3 AAG00534 Human sec  
861 20 87.0 73 4 AAU61284 Propionib  
862 20 87.0 73 4 AAU58953 Propionib  
863 20 87.0 73 6 ABM57803 Propionib  
864 20 87.0 73 6 ABM55472 Propionib  
865 20 87.0 73 7 ADB74547 Mycobacte  
866 20 87.0 74 4 AAU39327 Propionib  
867 20 87.0 74 4 ABM16610 Human ner  
868 20 87.0 74 6 ABM35846 Propionib  
869 20 87.0 75 4 AAU61506 Propionib  
870 20 87.0 75 4 AAU65615 Propionib  
871 20 87.0 75 6 ABM62134 Propionib  
872 20 87.0 75 6 ABM58025 Propionib  
873 20 87.0 75 6 ADA22879 Triticum  
874 20 87.0 76 4 AAU49429 Propionib  
875 20 87.0 77 4 AAU59016 Propionib  
876 20 87.0 77 4 AAU45424 Propionib  
877 20 87.0 77 6 ABM45948 Propionib  
878 20 87.0 77 6 ABM55535 Propionib  
879 20 87.0 77 6 ABM60716 Propionib  
880 20 87.0 77 6 ABM41943 Propionib  
881 20 87.0 77 6 ADA22882 Triticum  
882 20 87.0 78 4 AAU41878 Propionib  
883 20 87.0 78 6 ABM38397 Propionib  
884 20 87.0 78 6 AAR63593 MAP-Kinas  
885 20 87.0 80 2 AAY11722 Human 5'  
886 20 87.0 80 4 AAC00953 Human pol  
887 20 87.0 80 4 AAU39895 Propionib  
888 20 87.0 80 4 AAU44873 Propionib  
889 20 87.0 80 6 ABM36414 Propionib  
890 20 87.0 80 6 ABM41392 Propionib  
891 20 87.0 82 4 AAU66482 Propionib  
892 20 87.0 82 6 ABM63001 Propionib  
893 20 87.0 83 4 AAU53304 Propionib  
894 20 87.0 83 6 ABM40418 Human ORF  
895 20 87.0 83 6 ABM49823 Propionib  
896 20 87.0 84 4 AAU48564 Propionib  
897 20 87.0 84 4 AAU51507 Propionib  
898 20 87.0 84 4 AAU61007 Propionib  
899 20 87.0 84 6 ABM45083 Propionib  
900 20 87.0 84 6 ABM48026 Propionib

902 20 87.0 84 6 ABM63519 Propionib  
903 20 87.0 85 4 AAU67726 Propionib  
904 20 87.0 86 2 ABM64245 Propionib  
905 20 87.0 86 2 AAU66350 Cathepsin  
906 20 87.0 86 4 AAU15688 Peptide #  
907 20 87.0 86 4 AAU28192 Peptide #  
908 20 87.0 86 4 ABG29511 Peptide #  
909 20 87.0 86 4 ABG20098 Protein #  
910 20 87.0 86 4 AAU67867 Human bon  
911 20 87.0 86 4 AAU55482 Human liv  
912 20 87.0 86 4 ABG49511 Human bra  
913 20 87.0 86 4 AAU03424 Peptide #  
914 20 87.0 86 5 ABG37414 Human pep  
915 20 87.0 86 6 ABM64696 Propionib  
916 20 87.0 87 4 AAU01272 Human gen  
917 20 87.0 87 4 AAU60416 Propionib  
918 20 87.0 87 4 AAU57244 Human alb  
919 20 87.0 87 5 ABG63698 Human alb  
920 20 87.0 87 6 ABM56935 Propionib  
921 20 87.0 87 6 ABM53763 Propionib  
922 20 87.0 87 6 ADA48000 Rice prot  
923 20 87.0 88 2 AAU88828 Polypepti  
924 20 87.0 88 4 ABG50777 Human sec  
925 20 87.0 88 6 ABO45034 Novel hum  
926 20 87.0 88 7 ABO26514 Protein a  
927 20 87.0 88 7 ADE60508 Rat Prote  
928 20 87.0 89 2 AAR22429 Murine CP  
929 20 87.0 89 4 ABM44594 Mouse wou  
930 20 87.0 89 4 AAU45094 Propionib  
931 20 87.0 89 4 AAU41378 Propionib  
932 20 87.0 89 6 ABM82709 Murine MR  
933 20 87.0 89 6 ABM37897 Propionib  
934 20 87.0 89 6 ABM41613 Propionib  
935 20 87.0 90 4 AAU76109 Human col  
936 20 87.0 90 4 AAU55156 Propionib  
937 20 87.0 90 6 ABM51675 Propionib  
938 20 87.0 92 4 AAU66183 Propionib  
939 20 87.0 92 5 ABM78893 Tumour ne  
940 20 87.0 92 6 ABM62702 Propionib  
941 20 87.0 92 6 ABM66066 Propionib  
942 20 87.0 93 4 AAU30545 Novel hum  
943 20 87.0 93 7 ADC96253 E. faeciu  
944 20 87.0 94 5 ABM78934 Tumour ne  
945 20 87.0 94 5 ABM78891 Tumour ne  
946 20 87.0 94 5 ABM78892 Tumour ne  
947 20 87.0 96 2 ABP76895 N. gonorr  
948 20 87.0 96 2 AAU14540 Streptoco  
949 20 87.0 98 3 AAG00958 Human sec  
950 20 87.0 98 4 AAU47157 Propionib  
951 20 87.0 98 6 ABM43676 Propionib  
952 20 87.0 99 5 ABP33543 Human ORF  
953 20 87.0 101 6 ABP78296 Human ORF  
954 20 87.0 102 4 AAM88993 Human imm  
955 20 87.0 103 3 AAB41058 Human ORF  
956 20 87.0 103 3 AAG54132 Arabidops  
957 20 87.0 103 3 AAG26980 Arabidops  
958 20 87.0 103 4 AAU11211 Human pol  
959 20 87.0 103 6 ABM49349 Propionib  
960 20 87.0 104 4 AAB68492 Amino aci  
961 20 87.0 104 4 ABM67789 Drosophi1  
962 20 87.0 104 5 ABP06719 Human ORF  
963 20 87.0 104 5 ABP63770 Human ORF  
964 20 87.0 105 6 ABM58723 Human ORF  
965 20 87.0 105 6 ABM55242 Propionib  
966 20 87.0 106 4 AAU46300 Propionib  
967 20 87.0 106 5 ABP10289 Human ORF  
968 20 87.0 106 5 ABM05403 M. tuberc  
969 20 87.0 106 6 ABM42819 Propionib  
970 20 87.0 107 3 AAG54451 Zea mays  
971 20 87.0 110 3 AAG07125 Arabidops  
972 20 87.0 110 4 AAO00499 Human pol  
973 20 87.0 110 5 ABP34331 Human ORF

975 20 87.0 111 3 AAG58334 Arabidops  
976 20 87.0 111 4 AAM85333 Human imm  
977 20 87.0 111 4 AAU61097 Propionib  
978 20 87.0 111 6 ABM57616 Propionib  
979 20 87.0 113 2 AAR15677 SYNTH-9  
980 20 87.0 113 4 AAO09601 Human pol  
981 20 87.0 116 2 AAW64552 Human sto  
982 20 87.0 116 2 AAW59877 Amino aci  
983 20 87.0 116 2 AAW71627 Human hea  
984 20 87.0 116 5 ABB07624 Wheat nic  
985 20 87.0 116 6 ADA20759 Corn phos  
986 20 87.0 120 3 AAY66754 Membrane-  
987 20 87.0 120 3 AAB24077 Human PRO  
988 20 87.0 120 4 AAB65277 Human PRO  
989 20 87.0 120 5 ABP69105 Human POL  
990 20 87.0 120 5 AAU83640 Human PRO  
991 20 87.0 120 6 ABUS8092 Human PRO  
992 20 87.0 120 6 ABUS9170 Novel hum  
993 20 87.0 120 6 ABUS2682 Human sec  
994 20 87.0 120 6 ABUS6061 Human sec  
995 20 87.0 120 6 ABUS0787 Human PRO  
996 20 87.0 120 6 ABO33753 Novel hum  
997 20 87.0 120 6 ABUI3983 Human PRO  
998 20 87.0 120 6 ABUS2568 Novel hum  
999 20 87.0 120 6 ABUS9317 Human sec  
1000 20 87.0 120 8 ADD74799 Human PRO

# ALIGNMENTS

RESULT 1  
AA990711 standard; peptide; 4 AA.  
XX  
AC AAY90711;  
XX  
DT 14-AUG-2000 (first entry)  
XX  
DE Human albumin N-terminal metal binding site peptide SEQ ID NO:1.  
XX  
KW Human; albumin; metal binding site; detection; free radical damage;  
KW blood; Parkinson's disease; Alzheimer's disease; cataractogenesis;  
KW atherosclerosis; diabetes mellitus; ischaemia-reperfusion injury;  
KW toxicity.  
XX  
OS Homo sapiens.  
XX  
PN WO200020454-A1.  
XX  
PD 13-APR-2000.  
XX  
PF 01-OCT-1999; 99WO-US022746.  
XX  
PR 02-OCT-1998; 98US-00165961.  
XX  
PR 02-OCT-1998; 98US-0102962P.  
XX  
PA (DIAG-) DIAGNOSTIC MARKERS INC.  
XX  
PI Bar-Or D, Lau E;  
XX  
XX WPI; 2000-303746/26.  
XX  
XX Sensitive marker for detection of free radical damage comprising modified  
PT albumin, useful for detecting diseases associated with free radicals such  
PT as neurodegenerative diseases and cancers.  
XX  
XX Claim 15; Page 31; 40pp; English.  
XX  
XX The present invention describes a marker (I) for the detection of free  
CC radical damage, comprising albumin which is modified in a manner  
CC resulting in inhibition of metal binding capacity of the N-terminus. Also  
CC described are methods for detecting and quantifying (I). The methods are

CC useful for detecting diseases associated with free radicals including  
CC Parkinson's, Alzheimer's, cataractogenesis, atherosclerosis, diabetes  
CC mellitus, ischaemia-reperfusion injury and certain toxicities. (I) is  
CC useful as a biochemical tag, allowing for sensitive detection and  
CC measurement of the efficacy of clinical drugs and therapeutics which  
CC result in the generation of free radicals or which act to limit free  
CC radical damage. (I) is a marker for the existence and detection and/or  
CC measurement of free radical damage which is highly sensitive and present  
CC in a majority of human fluids and tissues. The present sequence  
CC represents the specifically claimed human albumin N-terminal metal  
CC binding site  
XX  
SQ Sequence 4 AA;  
Query Match 100.0%; Score 23; DB 3; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DAHK 4  
Db 1 DAHK 4  
RESULT 2  
AAB74365  
ID AAB74365 standard; peptide; 4 AA.  
XX  
AC AAB74365;  
XX  
DT 02-JUL-2001 (first entry)  
XX  
DE Reactive oxygen species inhibitory peptide.  
XX  
KW ROS; reactive oxygen species; metal binding; ischemia; neurodegenerative.  
XX  
OS Synthetic.  
XX  
PN WO200125265-A1.  
XX  
PD 12-APR-2001.  
XX  
PF 29-SEP-2000; 2000WO-US026952.  
XX  
PR 01-OCT-1999; 99US-0157404P.  
PR 13-JUN-2000; 2000US-0211078P.  
XX  
PA (BARO/) BAR-OR D.  
PA (CORT/) CORTIS C G.  
PA (LAUE/) LAU E.  
PA (RAON/) RAO N K R.  
PA (WINK/) WINKLER J V.  
PA (CROO/) CROOK W M.  
XX  
PI Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;  
XX  
XX WPI; 2001-328322/34.  
XX  
XX Metal binding peptide compounds prevent damage by reactive oxygen species  
PT in animal organs and tissues, useful for reperfusion, transplantation and  
PT treating e.g. ischemia, neurological and cardiovascular diseases.  
XX  
XX Example 10; Page 43; 124pp; English.  
XX  
XX The present invention relates to metal binding peptides that prevent  
CC damage by reactive oxygen. The peptides may be used for reperfusion an  
CC ischemic tissue or organ with cerebral or cardiovascular ischemia, for  
CC treating neurological trauma and for neurodegenerative disease. The  
CC present sequence is a reactive oxygen species inhibitory peptide  
XX  
SQ Sequence 4 AA;  
Query Match 100.0%; Score 23; DB 4; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 Db 1 DAHK 4

RESULT 3  
 AAB86898  
 ID AAB86898 standard; peptide; 4 AA.  
 AC AAB86898;  
 XX  
 DT 28-NOV-2001 (first entry)  
 XX  
 DE Transport molecule/ligand binding-associated peptide #44.  
 XX  
 KW Transport molecule; ligand; cancer treatment; autoimmune disease;  
 KW inflammation; infection.  
 XX  
 OS Synthetic.  
 XX  
 PN WO200168142-A1.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 13-MAR-2001; 2001WO-EP002833.  
 XX  
 PR 13-MAR-2000; 2000DE-01012120.  
 XX  
 PA (KTET-) KTB TUMORFORSCHUNGS GMBH.  
 XX  
 PI Kratz F;  
 XX  
 DR WPI; 2001-589998/66.  
 XX  
 PT New ligand, comprising therapeutic or diagnostic agent bonded non-covalently with substance having high affinity to transport molecule.  
 XX  
 PS Disclosure; Page 41; 74pp; German.  
 XX  
 CC This invention describes novel ligands which bind to transport molecules, comprising a therapeutic and/or diagnostic agent (A) non-covalently bonded via a linkage cleavable in vivo depending on pH and/or enzymatically with a substance (B) having an association constant KA to a transport molecule of above  $10^3 \text{ M}^{-1}$ , is new. The medicaments are especially useful for the treatment of cancers, autoimmune diseases, acute and chronic inflammation and infections caused by viruses or microorganisms. The diagnostic kits are useful for the detection of these illnesses and for the detection of the transport molecule and/or its distribution in vivo. The ligands have excellent solubility in the medium at the site of action and are easy and inexpensive to convert into adducts, as the interaction with the transport material is physical.  
 CC AAB86843-AAB86920 represent peptides used to illustrate the method of the invention  
 XX  
 SQ Sequence 4 AA;

Query Match 100.0%; Score 23; DB 4; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 Db 1 DAHK 4

RESULT 4  
 AAE14799  
 ID AAE14799 standard; peptide; 4 AA.  
 AC AAE14799;  
 XX

24-FEB-2003 (first entry)  
 Human serum albumin N-terminal metal binding peptide.  
 Reactive oxygen species; ROS; metal-binding peptide; angiogenesis; embryo implantation; endometriosis; tumour; hypertrophy; psoriasis; connective tissue disorder; ocular angiogenic disease; polyposis; cardiovascular disease; cerebral vascular disease; immune disorder; sepsis; obesity; acidosis; arthritis; asthma; autoimmune disease; cancer; cystic fibrosis; diabetes; hepatitis C; infertility; inflammation; inflammatory bowel disease; neurological disease; multiple sclerosis; pancreatitis; human; serum albumin.  
 KW  
 OS Homo sapiens.  
 XX  
 PN WO200264620-A2.  
 XX  
 PD 22-AUG-2002.  
 XX  
 PF 13-FEB-2002; 2002WO-US004275.  
 XX  
 PR 13-FEB-2001; 2001US-0268558P.  
 PR 22-MAR-2001; 2001US-00816679.  
 PR 04-APR-2001; 2001US-0281648P.  
 PR 11-APR-2001; 2001US-0283507P.  
 XX  
 PA (DMTB-) DMI BIOSCIENCES INC.  
 XX  
 PI Bar-Or D, Curtis CG, Lau E, Rao NKR, Winkler JV, Crook WM;  
 XX WPI; 2002-691590/74.  
 XX  
 PT New method for the inhibition of angiogenesis and the treatment of angiogenic disease, sepsis, and a disease involving acidosis, comprises the administration of a specified peptide or its salt.  
 PT  
 XX  
 PS Example 1; Page 41; 129pp; English.  
 XX  
 CC The invention relates to a method for reducing molecular, cellular and tissue damage done by reactive oxygen species (ROS) and also reducing concentration of a metal ion in an animal using specific metal-binding peptides and their derivatives that bind metal ions. The compounds of the invention are useful for inhibiting angiogenesis (including required for embryo implantation e.g. in endometriosis), and for treating angiogenic diseases, such as tumour (preferably a benign tumour), tumour metastasis, hypertrophy, connective tissue disorder, psoriasis, ocular angiogenic disease, cardiovascular disease, cerebral vascular disease, polyposis, obesity, immune disorder, sepsis, and a disease or condition involving acidosis. The compounds are also useful in the treatment of ARDS, aging, AIDS, arteriosclerosis (hypertension, senility and impotence), arthritis, asthma, autoimmune diseases, cancer, chronic granulomatous disease, cirrhosis, colitis, Crohn's disease, cystic fibrosis, neurodegenerative diseases, diabetes (diabetic retinopathy, renal disease, impotence and peripheral vascular disease), eye diseases, emphysema, head and traumatic brain injury, hepatitis C, infertility, inflammation, inflammatory bowel disease, metastasis, ischaemia, neoplastic diseases, neurological diseases, multiple sclerosis, pancreatitis, peripheral vascular disease, prion disease, pulmonary embolism, reperfusion, scleroderma, sepsis, shock, tissue damage, toxic reactions (e.g. poisoning (herbicide, transition metal, carbon monoxide, and antibiotic toxicity)). The present sequence is human serum albumin N-terminal peptide that binds Cu(II) and Ni(II) metals. The peptide and its derivatives are used in the invention

Query Match 100.0%; Score 23; DB 5; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 Db 1 DAHK 4

RESULT 5  
ABR39034  
ID ABR39034 standard; peptide; 4 AA.  
XX  
AC ABR39034;  
XX  
DT 10-MAY-2003 (first entry)  
XX  
DE Acylated polypeptide N-terminal extension peptide SEQ ID NO:35.  
XX  
XX Acylated, N-terminal extension.  
XX  
OS Synthetic.  
XX  
PN WO2003010186-A2.  
XX  
PD 06-FEB-2003.  
XX  
PF 18-JUL-2002; 2002WO-DK000502.  
XX  
PR 24-JUL-2001; 2001DK-00001141.  
XX  
PA (NOVO ) NOVO NORDISK AS.  
XX  
PI Diers I, Balschmidt P, Markussen J, Jonassen I, Egel-Mitani M;  
PI Kjeldsen TB;  
XX  
DR WPI; 2003-268032/26.  
XX  
XX Making polypeptides having at least one lysine residue in transformed  
PT host cells by expressing a precursor molecule of the desired polypeptide  
PT which is to be acylated and subsequently cleaved.  
XX  
PS Claim 31; Page 24; 42pp; English.  
XX  
CC The present invention describes making a polypeptide with at least one  
CC lysine residue being acylated in its epsilon-amino group, comprising  
CC culturing a host cell with a polynucleotide encoding and expressing a  
CC precursor molecule, separating the precursor from the culture broth,  
CC preferentially acylating the epsilon-amino group in the desired  
CC polypeptide, removing the N-terminal extension from the acylated  
CC precursor by enzymatic cleavage and isolating the acylated polypeptide.  
CC The precursor molecule comprises the desired polypeptide and an N-  
CC terminal extension cleavable from the desired polypeptide at a lysine  
CC cleavage site. The methods and compositions of the present invention are  
CC useful for the production of polypeptides in transformed host cells by  
CC expressing a precursor molecule of the desired polypeptide which is to be  
CC acylated and subsequently cleaved at a Lys cleavage site in a subsequent  
CC in vitro step. The present sequence represents a specifically claimed N-  
CC terminal extension peptide from the present invention  
XX  
SQ Sequence 4 AA;  
  
Query Match 100.0%; Score 23; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DAHK 4  
DB 1 DAHK 4  
  
RESULT 6  
ABP98620  
ID ABP98620 standard; peptide; 4 AA.  
XX  
AC ABP98620;  
XX  
DT 13-JUN-2003 (first entry)  
XX  
DE Cu-chelator peptide #1 for inhibiting copper-inactivation of APC.  
XX

KW anticoagulant; thrombolytic; antiinflammatory; antibacterial; antiulcer;  
KW immunosuppressive; antiasthmatic; antiparkinsonian; neuroleptic; asthma;  
KW antidepressant; antimanic; nootropic; dermatological; hypotensive;  
KW antiarteriosclerotic; antiallergic; activated protein C; APC; DVT;  
KW sepsis; coagulation disorder; inflammation; septic shock; hypertension;  
KW deep vein thrombosis; Parkinson's disease; schizophrenia; ulcer;  
KW manic depression; Huntington's disease; atherosclerosis; allergy.  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1. .4  
FT /note= "optionally D-form residues"  
XX  
XX WO2003007686-A2.  
XX  
PD 30-JAN-2003.  
XX  
XX 19-JUL-2002; 2002WO-US022951.  
XX  
PF 19-JUL-2001; 2001US-0307005P.  
XX  
PR 28-DEC-2001; 2001US-0344514P.  
XX  
XX (DMIB-) DMI BIOSCIENCES INC.  
XX  
XX Bar-Or D, Yukl RL;  
XX  
XX WPI; 2003-278307/27.  
XX  
XX Method for using active protein C (APC) comprising a copper chelator and  
PT protein C or protein C activator, useful for the treatment of coagulation  
PT disorders, inflammation, septic shock and deep vein thrombosis.  
XX  
XX Disclosure; Page 12; 68pp; English.  
XX  
XX The invention relates to a method of treating diseases treatable with  
CC activated protein C (APC) by inhibiting the inactivation of APC by copper  
CC (Cu) ions. The method includes the administration of a copper chelator,  
CC and APC, protein C (and/or an agent that increases synthesis of protein  
CC C), and/or an activator of protein C. Peptides ABP98620-ABP98624 are  
CC examples of Cu chelators that can be used in the method of the invention.  
CC The peptides are based on the sequence of high-affinity N-terminal Cu-  
CC binding motifs from serum albumins. The method can be used for treating  
CC animals in need of APC due to suffering from an acquired hypercoagulable  
CC state or an acquired protein C deficiency, sepsis, or a condition  
CC associated with intravascular coagulation. The method can also be used  
CC for preventing and treating coagulation disorders, inflammation, septic  
CC shock, deep vein thrombosis, asthma, Parkinson's disease, schizophrenia,  
CC manic depression, Huntington's disease, SLE, atherosclerosis,  
CC hypertension, ulcers and allergies  
XX  
SQ Sequence 4 AA;  
  
Query Match 100.0%; Score 23; DB 6; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 DAHK 4  
DB 1 DAHK 4  
  
RESULT 7  
ABP98473  
ID ABP98473 standard; peptide; 4 AA.  
XX  
AC ABP98473;  
XX  
DT 11-AUG-2003 (first entry)  
XX  
DE Amino acid sequence of a peptide.  
XX  
XX Mass spectrometry; spectrometer; mass filtering ion; charged ion;  
KW

KW human genome.  
 XX  
 OS Unidentified.  
 XX  
 PN EPL271138-A2.  
 XX  
 PD 02-JAN-2003.  
 XX  
 PF 21-JUN-2002; 2002EP-00254350.  
 XX  
 PR 21-JUN-2001; 2001GB-00015203.  
 PR 27-FEB-2002; 2002GB-00004601.  
 XX  
 PA (MTCR-) MICROMASS LTD.  
 XX  
 PI Bateman RH, Langridge JI, Hoyes JB, Wildgoose JL;  
 XX  
 DR WPI; 2003-334764/32.  
 XX  
 XX Mass spectrometry for medical applications, involves varying mass  
 PT filtered ions progressively so that ions having one charged state are  
 PT onwardly transmitted in preference to ions having different charge state.  
 XX  
 PS Disclosure; Fig 3a; 29pp; English.  
 XX  
 CC The specification describes a method of mass spectrometry, comprising  
 CC ions from an ion source which are separated according to their ion  
 CC mobility by a spectrometer. The ions are then filtered according to mass  
 CC to charge ratio. The mass filtering ions which are doubly charged, triply  
 CC charged, quadruply charged, and having five or more charges are  
 CC progressively varied so that ions having one charge state are onwardly  
 CC transmitted in preference to ions having different charge state. The  
 CC method is useful for performing mass spectrometry for the identification  
 CC of human genome for medical applications. ABP98451-74 represent peptides  
 CC derived from a graph of known relationship of flight time in a drift  
 CC region of a time of flight mass analyser versus drift time in an ion  
 CC mobility spectrometer for various doubly and singly charged ions  
 XX  
 SQ Sequence 4 AA;  
 Query Match 100.0%; Score 23; DB 6; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAHK 4  
 DB ||||  
 1 DAHK 4  
 RESULT 8  
 ABR39023  
 ID ABR39023 standard; peptide; 5 AA.  
 XX  
 AC ABR39023;  
 XX  
 DT 10-MAY-2003 (first entry)  
 XX  
 DE Acylated polypeptide N-terminal extension peptide SEQ ID NO:24.  
 XX  
 DE Acylated; N-terminal extension.  
 XX  
 KW Acylated; N-terminal extension.  
 XX  
 OS Synthetic.  
 XX  
 PN WO2003010186-A2.  
 XX  
 PD 06-FEB-2003.  
 XX  
 PF 18-JUL-2002; 2002WO-DK000502.  
 XX  
 PR 24-JUL-2001; 2001DK-00001141.  
 XX  
 PA (NOVO ) NOVO NORDISK AS.  
 XX

PI Diers I, Balschmidt P, Markussen J, Jonassen I, Egel-Mitani M;  
 PI Kjeldsen TB;  
 XX  
 DR WPI; 2003-268032/26.  
 XX  
 XX Making polypeptides having at least one lysine residue in transformed  
 PT host cells by expressing a precursor molecule of the desired polypeptide  
 PT which is to be acylated and subsequently cleaved.  
 XX  
 XX Claim 17; Page 22; 42pp; English.  
 PS  
 XX The present invention describes making a polypeptide with at least one  
 CC lysine residue being acylated in its epsilon-amino group, comprising a  
 CC culturing a host cell with a polynucleotide encoding and expressing a  
 CC precursor molecule, separating the precursor from the culture broth,  
 CC preferentially acylating the epsilon-amino group in the desired  
 CC polypeptide, removing the N-terminal extension from the acylated  
 CC precursor by enzymatic cleavage and isolating the acylated polypeptide.  
 CC The precursor molecule comprises the desired polypeptide and an N-  
 CC terminal extension cleavable from the desired polypeptide at a lysine  
 CC cleavage site. The methods and compositions of the present invention are  
 CC useful for the production of polypeptides in transformed host cells by  
 CC expressing a precursor molecule of the desired polypeptide which is to be  
 CC acylated and subsequently cleaved at a lys cleavage site in a subsequent  
 CC in vitro step. The present sequence represents a specifically claimed N-  
 CC terminal extension peptide from the present invention  
 XX  
 SQ Sequence 5 AA;  
 Query Match 100.0%; Score 23; DB 6; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAHK 4  
 DB ||||  
 2 DAHK 5  
 RESULT 9  
 AAW23611  
 ID AAW23611 standard; peptide; 6 AA.  
 XX  
 AC AAW23611;  
 XX  
 DT 11-FEB-1998 (first entry)  
 XX  
 DE Prolactin antagonist (SI77A substituted C-terminal fragment).  
 XX  
 KW Prolactin antagonist; phosphorylation; hyperprolactinaemia; prolactinoma;  
 KW prostate cancer; tumour; T-lymphoma; infertility; lactation; miscarriage;  
 KW ovulation; antibody; therapy; rat.  
 XX  
 OS Rattus sp.  
 OS Synthetic.  
 XX  
 PN WO9727865-A1.  
 XX  
 PD 07-AUG-1997.  
 XX  
 PF 30-JAN-1997; 97WO-US001435.  
 XX  
 PR 31-JAN-1996; 96US-00594809.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Walker AM;  
 XX  
 DR WPI; 1997-402308/37.  
 XX  
 XX Substituted prolactin peptide(s) and proteins having an amino acid  
 PT substitution for serine in the C-terminal - useful as prolactin  
 PT antagonists, e.g. for treating prolactin dependent cancers.  
 XX



PS Claim 4; Page 11; 158pp; English.

XX This peptide comprises a rat prolactin C-terminal fragment (amino acid  
 CC residues 175-180) substituted at position 177 (serine in the native  
 CC sequence) by alanine. It has prolactin antagonist activity, antagonising  
 CC the stimulation of T lymphoma cell growth in the presence of non-  
 CC phosphorylated prolactin. A method is claimed for preparation of  
 CC recombinant prolactin substitution peptides (see AAT74327-32). The  
 CC products (see AAW23607-19) can be used for the treatment of prolactin  
 CC dependent cancers and can inhibit T-lymphoma cell proliferation. They are  
 CC also useful for treatment of prolactinoma, infertility related to  
 CC abnormal prolactin regulation, some forms of prostatic cancer,  
 CC miscarriage and ovulation irregularities, as well as in assays to measure  
 CC levels of non-phosphorylated and phosphorylated prolactin as an indicator  
 CC of reproductive pathologies and presence or status of a prolactin-  
 CC dependent tumour, and to raise polyclonal and monoclonal antibodies  
 CC  
 XX Sequence 6 AA;

Query Match 100.0%; Score 23; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 Db 2 DAHK 5

RESULT 10  
 AAW23634  
 ID AAW23634 standard; peptide; 6 AA.  
 XX AAW23634;  
 AC  
 XX  
 DT 11-FEB-1998 (first entry)  
 XX  
 DE Human prolactin peptide (aal77-182, S179A substituted).  
 KW Prolactin antagonist; phosphorylation; hyperprolactinaemia; prolactinoma;  
 KW prostate cancer; tumour; T-lymphoma; infertility; lactation; therapy;  
 KW human.  
 XX Homo sapiens.  
 OS Synthetic.  
 OS  
 XX WO9727865-A1.  
 PN  
 XX  
 PD 07-AUG-1997.  
 XX  
 XX 30-JAN-1997; 97WO-US001435.  
 PF  
 XX 31-JAN-1996; 96US-00594809.  
 PR  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Walker AM;  
 PI  
 XX WPI; 1997-402308/37.  
 DR  
 XX Substituted prolactin peptide(s) and proteins having an amino acid  
 PT substitution for serine in the C-terminal - useful as prolactin  
 PT antagonists, e.g. for treating prolactin dependent cancers.  
 XX  
 XX Disclosure; Page 14; 158pp; English.  
 PS  
 XX This peptide comprises a human prolactin C-terminal fragment (amino acid  
 CC residues 177-182) substituted at position 179 (serine in the native  
 CC sequence) by alanine. Claimed substituted prolactin peptides and proteins  
 CC (see AAW23607-19) have antagonistic activity with wild-type prolactin.  
 CC They comprise substitution and monophosphorylated C-terminal fragments of  
 CC prolactin containing a substituted serine residue (177 for rat, 179 for  
 CC human). A method is claimed for preparation of recombinant prolactin  
 CC substitution peptides (see AAT74327-32). The products can be used for the

CC treatment prolactin dependent cancers and can inhibit T-lymphoma cell  
 CC proliferation. They are also useful for the treatment of prolactinoma,  
 CC infertility related to abnormal prolactin regulation, some forms of  
 CC prostatic cancer, ovulation irregularities and miscarriage, as well as in  
 CC assays to measure levels of non- phosphorylated and phosphorylated  
 CC prolactin as an indicator of reproductive pathologies and presence or  
 CC status of a prolactin- dependent tumour, and to raise polyclonal and  
 CC monoclonal antibodies  
 XX  
 SQ Sequence 6 AA;

Query Match 100.0%; Score 23; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 Db 2 DAHK 5

RESULT 11  
 ABR39046  
 ID ABR39046 standard; peptide; 7 AA.  
 XX  
 AC ABR39046;  
 XX  
 XX 10-MAY-2003 (first entry)  
 DT  
 XX  
 DE Acylated polypeptide N-terminal extension peptide SEQ ID NO:47.  
 XX  
 KW Acylated; N-terminal extension.  
 XX  
 OS Synthetic.  
 OS  
 XX WO2003010186-A2.  
 PN  
 XX 06-FEB-2003.  
 PD  
 XX 18-JUL-2002; 2002WO-DK000502.  
 PF  
 XX 24-JUL-2003; 2001DK-00001141.  
 PR  
 XX (NOVO ) NOVO NORDISK AS.  
 PA  
 XX Diers I, Balschmidt P, Markussen J, Jonassen I, Egel-Mitani M;  
 PI Kjeldsen TB;  
 XX  
 XX WPI; 2003-268032/26.

XX Making polypeptides having at least one lysine residue in transformed  
 PT host cells by expressing a precursor molecule of the desired polypeptide  
 PT which is to be acylated and subsequently cleaved.  
 XX  
 XX Claim 17; Page 22; 42pp; English.  
 PS  
 XX The present invention describes making a polypeptide with at least one  
 CC lysine residue being acylated in its epsilon-amino group, comprising  
 CC culturing a host cell with a polynucleotide encoding and expressing a  
 CC precursor molecule, separating the precursor from the culture broth,  
 CC preferentially acylating the epsilon-amino group in the desired  
 CC polypeptide, removing the N-terminal extension from the acylated  
 CC precursor by enzymatic cleavage and isolating the acylated polypeptide.  
 CC The precursor molecule comprises the desired polypeptide and an N-  
 CC terminal extension cleavable from the desired polypeptide at a lysine  
 CC cleavage site. The methods and compositions of the present invention are  
 CC useful for the production of polypeptides in transformed host cells by  
 CC expressing a precursor molecule of the desired polypeptide which is to be  
 CC acylated and subsequently cleaved at a lys cleavage site in a subsequent  
 CC in vitro step. The present sequence represents a specifically claimed N-  
 CC terminal extension peptide from the present invention  
 XX  
 SQ Sequence 7 AA;



Query Match 100.0%; Score 23; DB 6; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;

QY 1 DAHK 4  
 DB 4 DAHK 7

RESULT 12  
 AAY90712  
 ID AAY90712 standard; peptide; 8 AA.

XX AC AAY90712;  
 XX DT 14-AUG-2000 (first entry)  
 XX DE Human albumin N-terminal octapeptide SEQ ID NO:2.

XX KW Human; albumin; metal binding site; detection; free radical damage;  
 KW blood; Parkinson's disease; Alzheimer's disease; cataractogenesis;  
 KW atherosclerosis; diabetes mellitus; ischaemia-reperfusion injury;  
 KW toxicity.

XX OS Homo sapiens.  
 XX FN WO200020454-A1.

XX PD 13-APR-2000.

XX PF 01-OCT-1999; 99WO-US022746.

XX PR 02-OCT-1999; 98US-00165961.

XX PR 02-OCT-1999; 98US-01029622.

XX PA (DIAG-) DIAGNOSTIC MARKERS INC.

XX PI Bar-Or D, Lau E;

XX DR WPI; 2000-303746/26.

XX PT Sensitive marker for detection of free radical damage comprising modified  
 PT albumin, useful for detecting diseases associated with free radicals such  
 PT as neurodegenerative diseases and cancers.

XX PS Example 1; Page 16; 40pp; English.

XX CC The present invention describes a marker (I) for the detection of free  
 CC radical damage, comprising albumin which is modified in a manner  
 CC resulting in inhibition of metal binding capacity of the N-terminus. Also  
 CC described are methods for detecting and quantifying (I). The methods are  
 CC useful for detecting diseases associated with free radicals including  
 CC Parkinson's, Alzheimer's, cataractogenesis, atherosclerosis, diabetes  
 CC mellitus, ischaemia-reperfusion injury and certain toxicities. (I) is  
 CC useful as a biochemical tag, allowing for sensitive detection and  
 CC measurement of the efficacy of clinical drugs and therapeutics which  
 CC result in the generation of free radicals or which act to limit free  
 CC radical damage. (I) is a marker for the existence and detection and/or  
 CC measurement of free radical damage which is highly sensitive and present  
 CC in a majority of human fluids and tissues. The present sequence  
 CC represents the human albumin N-terminal octapeptide which is used in  
 CC examples from the present invention to measure cobalt binding

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 3; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;

QY 1 DAHK 4  
 DB 1 DAHK 4

# RESULT 13

ABG70867  
 ID ABG70867 standard; peptide; 8 AA.

XX AC ABG70867;

XX DT 28-NOV-2002 (first entry)

XX DE Fluorescent binding peptide for determination of albumin in urine.

XX KW Analyte concentration; polarised light; binding ligand; blood test;  
 KW blood cell lysis; albumin; urine.

XX OS Homo sapiens.

XX FN WO200244721-A1.

XX PD 06-JUN-2002.

XX PF 30-NOV-2001; 2001WO-N0000480.

XX PR 01-DEC-2000; 2000NO-00006130.

XX PA (SUND/) SUNDREHAGEN E.

XX PI Sundrehagen E;

XX DR WPI; 2002-691469/74.

XX PT Determination of concentration of at least one analyte in a test sample  
 PT involves mixing the sample with a single reagent, irradiating the mixture  
 PT and calculating the concentration of the analyte.

XX PS Example 10; Page 43; 78pp; English.

XX CC The invention relates to the determination of concentration of at least  
 CC one analyte in a test sample or an aliquot of a test sample of a complex  
 CC biological fluid involves: (i) mixing the sample or aliquot of the sample  
 CC with one single reagent such as a solid, solution or premixed solution to  
 CC form a mixture (ii) irradiating the mixture with polarised light which  
 CC permits the excitation of the fluorescent molecules (iii) measuring the  
 CC polarisation of the emitted light, and (iv) calculating the  
 CC concentration(s) of the analyte(s). The reagent is provided in one single  
 CC container or compartment of a container and no other reagent is added  
 CC during the performance of the method. The reagent further comprises at  
 CC least one type of binding molecule with specific affinity for at least  
 CC one of the analytes and either fluorescent moieties covalently linked to  
 CC the binding molecules or fluorescent analogues, fluorescent fragments or  
 CC fluorescent derivatives of the analyte(s). The method is used for the  
 CC determination of concentration of at least one analyte in a test sample  
 CC or an aliquot of a test sample of a complex biological fluid.

XX CC particularly for the determination of concentrations of clinically  
 CC related substances in samples of biological material from a living  
 CC organism e.g. plants, insects, birds and animals such as mammals (e.g.  
 CC primates or humans). The method involves use of stable, durable reagents;  
 CC is carried out in very few (preferably just one single container); does  
 CC not require any significant pipette work. The method can be carried out  
 CC on blood tests after or with simultaneous lysis of the blood cells. The  
 CC method is a sensitive specific measurement method. The method is carried  
 CC out at constant temperature by use of correction algorithms empirically  
 CC generated by temperature's influence on test solutions with known  
 CC concentration of the analyte. The present sequence is a fluorescent  
 CC peptide for determination of albumin in urine (it is the N-terminus of  
 CC human albumin) using the method of the invention

XX SQ Sequence 8 AA;

Query Match 100.0%; Score 23; DB 5; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.4e+06; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0;

QY 1 DAHK 4

Db ||||  
1 DAHK 4

## RESULT 14

AAE13134  
ID AAE13134 standard; peptide; 9 AA.

XX  
AC AAE13134;

XX  
DT 28-JAN-2002 (first entry)

XX  
DE Human albumin (HA) peptide.

XX  
KW Human; albumin; HA; fusion protein; therapeutic protein; vulnary;  
KW immune system disorder; transplant rejection; blood related disorder;  
KW myocardial infarction; hyperproliferative disorder; glomerulonephritis;  
KW childhood acute myeloid leukemia; cardiovascular disorder; arrhythmia;  
KW respiratory disorder; gene therapy; non-allergic rhinitis; noctropic;  
KW neurological disease; Alzheimer's disease; reproductive system disorder;  
KW endocrine disorder; pheochromocytoma; infectious disease; antiarrhythmic;  
KW measles; gastrointestinal disorder; irritable bowel syndrome; syphilis;  
KW wound healing; antiinflammatory; immunosuppressive; neuroprotective;  
KW cardiant; cytostatic; antileukaemic; antineumatic; antimicrobial;  
KW renal disorder.

XX  
OS Homo sapiens.

XX  
PN WO200179443-A2.

XX  
PD 25-OCT-2001.

XX  
PF 12-APR-2001; 2001WO-US011924.

XX  
PR 12-APR-2000; 2000US-0229358P.

XX  
PR 23-APR-2000; 2000US-0199384P.

XX  
PR 21-DEC-2000; 2000US-0256931P.

XX  
XX (HUMA-) HUMAN GENOME SCI INC.

XX  
XX Rosen CA, Haseltine WA;

XX  
DR WPI; 2001-616754/71.

XX  
PT Albumin fusion proteins comprising a therapeutic protein and albumin,  
PT useful in the treating immune system disorders (e.g. transplant  
PT rejection), blood related disorders (e.g. myocardial infarction) and  
PT hyperproliferative disorders.

XX  
PS Example 2; Page 232; 380pp; English.

XX  
CC The invention relates to albumin fusion proteins comprising therapeutic  
CC protein and human albumin (HA). Therapeutic protein fused to albumin have  
CC an extended shelf-life. The albumin fusion proteins are useful in the  
CC treatment, prevention, diagnosis and/or detection of diseases, disorders  
CC such as immune system disorders (e.g. transplant rejection), blood  
CC related disorders (e.g. myocardial infarction), hyperproliferative  
CC disorders (e.g. childhood acute myeloid leukemia), renal disorders (e.g.  
CC glomerulonephritis), cardiovascular disorders (e.g. arrhythmias),  
CC respiratory disorders (e.g. non-allergic rhinitis), neurological diseases  
CC (e.g. Alzheimer's disease), endocrine disorders (e.g. pheochromocytoma),  
CC reproductive system disorders (e.g. syphilis), infectious diseases (e.g.  
CC measles), gastrointestinal disorders (e.g. irritable bowel syndrome) and  
CC wound healing. Nucleic acids encoding albumin fusion protein is used in  
CC gene therapy. The present sequence is human albumin (HA) peptide

XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 4; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4

Db ||||  
1 DAHK 4

## RESULT 15

ABR39047  
ID ABR39047 standard; peptide; 9 AA.

XX  
AC ABR39047;

XX  
DT 10-MAY-2003 (first entry)

XX  
DE Acylated polypeptide N-terminal extension peptide SEQ ID NO:48.

XX  
KW Acylated; N-terminal extension.

XX  
OS Synthetic.

XX  
PN WO2003010186-A2.

XX  
PD 06-FEB-2003.

XX  
PF 18-JUL-2002; 2002WO-DK000502.

XX  
PR 24-JUL-2001; 2001DK-00001141.

XX  
XX (NOVO ) NOVO NORDISK AS.

XX  
XX Diers I, Balschmidt P, Markussen J, Jonassen I, Egel-Mitani M;

XX  
PI Kjeldsen TB;

XX  
DR WPI; 2003-268032/26.

XX  
PT Making polypeptides having at least one lysine residue in transformed  
PT host cells by expressing a precursor molecule of the desired polypeptide  
PT which is to be acylated and subsequently cleaved.

XX  
PS Claim 17; Page 22; 42pp; English.

XX  
CC The present invention describes making a polypeptide with at least one  
CC lysine residue being acylated in its epsilon-amino group, comprising a  
CC culturing a host cell with a polynucleotide encoding and expressing a  
CC precursor molecule, separating the precursor from the culture broth,  
CC preferentially acylating the epsilon-amino group in the desired  
CC polypeptide, removing the N-terminal extension from the acylated  
CC precursor by enzymatic cleavage and isolating the acylated polypeptide.  
CC The precursor molecule comprises the desired polypeptide and an N-  
CC terminal extension cleavable from the desired polypeptide at a lysine  
CC cleavage site. The methods and compositions of the present invention are  
CC useful for the production of polypeptides in transformed host cells by  
CC expressing a precursor molecule of the desired polypeptide which is to be  
CC acylated and subsequently cleaved at a Lys cleavage site in a subsequent  
CC in vitro step. The present sequence represents a specifically claimed N-  
CC terminal extension peptide from the present invention

XX  
SQ Sequence 9 AA;

Query Match 100.0%; Score 23; DB 6; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.4e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4

Db ||||  
6 DAHK 9

Search completed: September 9, 2004, 23:45:53  
Job time : 191 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 9, 2004, 23:41:38 ; Search time 39 Seconds

(without alignments)  
9.866 Million cell updates/sec

Title: US-10-076-071-1

Perfect score: 23

Sequence: 1 DAHK 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR\_78:\*

1: PIR1:\*

2: PIR2:\*

3: PIR3:\*

4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	87	2	C81890
2	23	100.0	92	2	T44734
3	23	100.0	94	2	AH0375
4	23	100.0	100	2	G86805
5	23	100.0	102	2	E75528
6	23	100.0	104	1	G43258
7	23	100.0	109	2	T45101
8	23	100.0	112	2	G97473
9	23	100.0	116	2	C82906
10	23	100.0	118	2	B90155
11	23	100.0	121	2	T36836
12	23	100.0	122	2	C70965
13	23	100.0	122	2	C75371
14	23	100.0	124	2	T08427
15	23	100.0	125	2	D81138
16	23	100.0	136	2	T39439
17	23	100.0	140	1	H8FGR
18	23	100.0	149	2	A47054
19	23	100.0	151	1	RGSHP
20	23	100.0	155	2	A82841
21	23	100.0	168	2	C33601
22	23	100.0	168	2	C37314
23	23	100.0	170	2	T11964
24	23	100.0	175	2	T09249
25	23	100.0	175	2	PH0261
26	23	100.0	179	2	AH3630
27	23	100.0	187	2	E89961
28	23	100.0	191	2	A96765
29	23	100.0	196	2	A39223

30	23	100.0	205	2	T18215
31	23	100.0	207	1	S31011
32	23	100.0	207	2	JS0718
33	23	100.0	209	2	E75600
34	23	100.0	211	2	T23696
35	23	100.0	211	2	F84467
36	23	100.0	212	2	B83543
37	23	100.0	216	2	D98240
38	23	100.0	216	2	B97992
39	23	100.0	218	1	VHVUSS
40	23	100.0	222	2	F95029
41	23	100.0	223	2	E64205
42	23	100.0	224	2	S02216
43	23	100.0	226	2	F83307
44	23	100.0	229	2	B95287
45	23	100.0	229	2	AH3045
46	23	100.0	230	2	JC5418
47	23	100.0	230	2	T12872
48	23	100.0	231	2	A35793
49	23	100.0	233	2	A23729
50	23	100.0	235	2	A49762
51	23	100.0	235	2	H82262
52	23	100.0	236	2	C75181
53	23	100.0	236	2	H71032
54	23	100.0	237	2	S73504
55	23	100.0	238	1	S44444
56	23	100.0	239	2	AI3013
57	23	100.0	245	2	S64105
58	23	100.0	256	2	F85505
59	23	100.0	256	2	F90654
60	23	100.0	262	2	F83498
61	23	100.0	262	2	TS2037
62	23	100.0	271	2	D90924
63	23	100.0	271	2	H85772
64	23	100.0	271	2	A64923
65	23	100.0	277	2	I37552
66	23	100.0	280	2	JE0217
67	23	100.0	283	2	S73524
68	23	100.0	285	2	F71076
69	23	100.0	285	2	F98270
70	23	100.0	286	2	F82881
71	23	100.0	289	2	AH0112
72	23	100.0	290	2	T21198
73	23	100.0	292	2	A64073
74	23	100.0	298	1	TVBY8
75	23	100.0	299	2	C97102
76	23	100.0	305	2	S40927
77	23	100.0	310	2	T29355
78	23	100.0	319	2	AI2125
79	23	100.0	324	2	AE3650
80	23	100.0	326	2	T04344
81	23	100.0	330	2	G95134
82	23	100.0	330	2	B98003
83	23	100.0	331	2	F86835
84	23	100.0	333	1	A38094
85	23	100.0	336	2	A82165
86	23	100.0	343	1	E70477
87	23	100.0	343	2	AB0197
88	23	100.0	344	2	S38939
89	23	100.0	344	2	S59043
90	23	100.0	345	1	B46113
91	23	100.0	345	2	S36959
92	23	100.0	347	2	E89788
93	23	100.0	347	2	T17645
94	23	100.0	350	2	A40459
95	23	100.0	351	2	T18066
96	23	100.0	351	2	T42421
97	23	100.0	358	2	D96722
98	23	100.0	360	2	C64628
99	23	100.0	360	2	D71888
100	23	100.0	361	2	T00437
101	23	100.0	362	2	D72734
102	23	100.0			

hypothetical prote  
probable phosphoe  
yafe protein - Esc  
butyrate-acetoacet  
hypothetical prote  
hypothetical prote  
hypothetical prote  
probable hydrolase  
conserved hypothet  
nucleocapsid prote  
transaldolase fami  
deoxyribose-phosph  
deoxyribose-phosph  
probable hydrolase  
probable hydrolase  
hydrolase [impor  
somatolactin - Sen  
somatolactin - Jap  
somatolactin - Jap  
somatolactin - Jap  
somatolactin - Jap  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
degV protein homol  
protein disulfide-  
tolQ Protein [impo  
probable membrane  
unknown [imported]  
probable biotin sy  
hypothetical prote  
14-3-3 regulatory  
probable lipoprote  
probable lipoprote  
hypothetical prote  
OX40 homolog - hum  
28k surface antige  
probable lipoprote  
hypothetical prote  
tolQ protein [impo  
hypothetical prote  
probable membrane  
hypothetical prote  
D-ribose-binding p  
protein kinase (EC  
hypothetical prote  
hypothetical prote  
hypothetical prote  
hypothetical prote  
oxidoreductase (EC  
peroxidase (EC 1.1  
acetoaldehyde dehydrogen  
hypothetical prote  
D-lactate dehydrog  
transcription regu  
GTP-binding protei  
beta-N-acetylhexos  
probable cathepsin  
spilling factor SR  
protein kinase (EC  
dopamine receptor  
hypothetical prote  
hypothetical prote  
nuclear phosphopro  
hypothetical prote  
hypothetical prote  
lipid A disacchari  
lipid-a-disacchari  
probable protein d  
probable histidine

103	23	100.0	366	2	B69949	phage-related prot	176	23	100.0	502	2	T36589	probable transmembr
104	23	100.0	368	2	T23315	hypothetical prote	177	23	100.0	502	2	A70985	probable polyketid
105	23	100.0	372	2	D87642	conserved hypotet	178	23	100.0	510	1	I64162	mvin protein homol
106	23	100.0	372	2	T25717	hypothetical prote	179	23	100.0	510	2	G72464	hypothetical prote
107	23	100.0	374	2	A37282	52K active chromat	180	23	100.0	518	2	B83439	hypothetical prote
108	23	100.0	379	2	T04645	hypothetical prote	181	23	100.0	519	2	G97560	probable glucose-1
109	23	100.0	388	2	C69420	GTP-binding protei	182	23	100.0	522	2	AC3374	probable sugar kin
110	23	100.0	389	1	SAVL71	large surface anti	183	23	100.0	527	2	AC2380	type I restriction
111	23	100.0	389	2	F69594	8-amino-7-oxonon	184	23	100.0	527	2	T15258	hypothetical prote
112	23	100.0	390	2	JS0296	transposase - Stap	185	23	100.0	534	2	E84590	hypothetical prote
113	23	100.0	391	2	C87615	acyltransferase, p	186	23	100.0	535	2	S40461	t-complex-type mol
114	23	100.0	412	2	A86225	protein T12M4.7 [i	187	23	100.0	540	2	T26445	hypothetical prote
115	23	100.0	414	2	G69536	group II decarboxy	188	23	100.0	545	2	AB0290	probable membrane
116	23	100.0	420	2	S19707	site-specific DNA-	189	23	100.0	548	2	H82234	probable glutamate
117	23	100.0	420	2	D86617	CT857 hypothetical	190	23	100.0	549	2	H96944	arginine degradati
118	23	100.0	420	2	S36444	hygromycin phospho	191	23	100.0	550	2	AB3136	MFS permease [impo
119	23	100.0	420	2	E72006	probable im protei	192	23	100.0	552	2	B98152	hypothetical prote
120	23	100.0	421	1	HQDVIV	cytochrome-c3 hydr	193	23	100.0	558	2	T50742	protoporphyrin IX
121	23	100.0	422	2	G81532	Na+/H+ antiporter,	194	23	100.0	570	2	F70844	probable fusion pr
122	23	100.0	424	1	B49851	protochlorophyllid	195	23	100.0	595	2	T39228	beta-transducin -
123	23	100.0	425	2	T50355	hypothetical prote	196	23	100.0	601	2	H81282	probable translati
124	23	100.0	427	2	D81725	Na+/H+ antiporter,	197	23	100.0	601	2	T15260	hypothetical prote
125	23	100.0	428	1	CTBSBA	site-specific DNA-	198	23	100.0	605	2	S43568	beta transducin ho
126	23	100.0	428	2	D81255	histidinol dehydro	199	23	100.0	608	2	T51217	hypothetical prote
127	23	100.0	429	2	A33309	uterine milk prote	200	23	100.0	609	1	ABHUS	serum albumin prec
128	23	100.0	430	2	T37198	hypothetical prote	201	23	100.0	614	2	D87410	iod protein [impo
129	23	100.0	431	2	H82237	histidinol dehydro	202	23	100.0	620	2	S55086	probable membrane
130	23	100.0	436	2	T39299	probable proteosom	203	23	100.0	620	2	D86903	asparagine synthas
131	23	100.0	437	2	C97020	argininosuccinate	204	23	100.0	631	2	T33559	hypothetical prote
132	23	100.0	440	2	A70067	NDP-sugar dehydrog	205	23	100.0	668	2	B86831	hypothetical prote
133	23	100.0	441	2	H83763	6-phospho-beta-glu	206	23	100.0	686	2	T10548	hypothetical prote
134	23	100.0	441	2	E96666	hypothetical prote	207	23	100.0	695	2	A87494	topoisomerase IV,
135	23	100.0	442	1	DYXLD2	dopamine receptor	208	23	100.0	699	2	AC3594	DNA topoisomerase
136	23	100.0	442	2	T06669	hypothetical prote	209	23	100.0	702	2	H84189	lipote protein li
137	23	100.0	443	2	D86183	hypothetical prote	210	23	100.0	702	2	H90757	probable oxidoredu
138	23	100.0	445	2	B65221	probable amino aci	211	23	100.0	702	2	F85621	probable oxidoredu
139	23	100.0	445	2	A91266	probable amino aci	212	23	100.0	702	2	C64835	hypothetical prote
140	23	100.0	445	2	F86106	probable amino aci	213	23	100.0	703	2	T48600	kinase-like protei
141	23	100.0	445	2	AF1022	probable amino aci	214	23	100.0	717	2	F82613	VacB protein XF198
142	23	100.0	446	2	D70597	probable signal pe	215	23	100.0	727	2	H69724	DNA topoisomerase
143	23	100.0	447	2	T34992	probable lipoprote	216	23	100.0	730	2	T05345	hypothetical prote
144	23	100.0	449	2	S16319	secretin receptor	217	23	100.0	731	2	S29870	DNA-binding protei
145	23	100.0	452	2	S27611	agglutination prot	218	23	100.0	743	2	S48917	probable regulator
146	23	100.0	456	2	S31125	26S proteasome reg	219	23	100.0	745	2	G84995	VacB protein [impo
147	23	100.0	457	2	AG2699	magnesium transpor	220	23	100.0	745	2	D96829	homeobox protein (
148	23	100.0	457	2	G97481	mg2+ transport pro	221	23	100.0	747	2	S71478	homeotic protein A
149	23	100.0	458	2	A75386	conserved hypotet	222	23	100.0	750	2	AB0708	catalase (EC 1.11.
150	23	100.0	459	2	AD1787	lysine decarboxyla	223	23	100.0	752	2	T09649	delta-1-pyrroline-
151	23	100.0	459	2	AE1411	lysine decarboxyla	224	23	100.0	752	2	F81203	maltose phosphoryl
152	23	100.0	464	2	C69356	conserved hypotet	225	23	100.0	752	2	C81781	probable maltose p
153	23	100.0	467	2	AE0735	probable bacteriop	226	23	100.0	753	2	A39129	catalase (EC 1.11.
154	23	100.0	467	2	AF0621	probable prophage	227	23	100.0	753	2	B85782	catalase, hydrolase
155	23	100.0	469	1	A39358	histidinol dehydro	228	23	100.0	753	2	F90933	catalase, hydrolase
156	23	100.0	470	1	WZBEA4	transcription acti	229	23	100.0	754	2	AP2849	methyl-accepting c
157	23	100.0	470	1	B42746	transcription acti	230	23	100.0	763	2	F96693	hypothetical prote
158	23	100.0	473	2	A38627	gamma-aminobutyric	231	23	100.0	765	2	T14564	inorganic diphosph
159	23	100.0	478	2	AC3386	glucose inhibited	232	23	100.0	766	2	S61424	inorganic diphosph
160	23	100.0	481	2	T37505	hypothetical prote	233	23	100.0	768	2	D97626	hypothetical prote
161	23	100.0	481	2	AG2781	glucose inhibited	234	23	100.0	770	2	T04792	hypothetical prote
162	23	100.0	483	2	H87492	YjeF family protei	235	23	100.0	783	2	AB3592	exoribonuclease [i
163	23	100.0	484	2	F64554	guanosine-5'-triph	236	23	100.0	784	2	AG2736	exoribonuclease RN
164	23	100.0	484	2	F71954	guanosine-5'-triph	237	23	100.0	786	2	E97517	hypothetical prote
165	23	100.0	485	1	ANHU	angiotensin precur	238	23	100.0	786	2	G96940	hypothetical prote
166	23	100.0	485	2	D87478	coniferyl aldehyde	239	23	100.0	787	2	T05617	hypothetical prote
167	23	100.0	490	1	A43492	surface glycoprote	240	23	100.0	789	2	S28359	androgen-regulated
168	23	100.0	491	1	VGXPLV	surface glycoprote	241	23	100.0	791	2	G81109	ribonuclease II fa
169	23	100.0	493	2	C86565	oligopeptide perme	242	23	100.0	791	2	B81906	probable ribonucle
170	23	100.0	493	2	D72059	peptide ABC transp	243	23	100.0	791	2	C82940	hypothetical prote
171	23	100.0	494	2	JH0665	catechol oxidase (	244	23	100.0	799	2	G87378	phenylalanyl-trna
172	23	100.0	494	2	A48133	pre-mRNA splicing	245	23	100.0	803	2	F90485	hypothetical prote
173	23	100.0	498	2	T39077	hypothetical prote	246	23	100.0	808	2	T16564	hypothetical prote
174	23	100.0	498	2	T10316	global transactiva	247	23	100.0	810	2	C70791	probable ponA', pro
175	23	100.0	500	2	B81250	probable site-spec	248	23	100.0	812	2	AH1049	ribonuclease R (RN

249	23	100.0	814	1	KXBY	102	23	100.0	322	23	100.0	4861	2	S71752	giant protein p619
250	23	100.0	821	2	C82055	103	23	100.0	323	23	100.0	4957	2	T03455	ALR protein - huma
251	23	100.0	822	2	T51049	104	23	100.0	324	23	100.0	5262	2	T03454	ALR protein - huma
252	23	100.0	825	2	T26706	105	20	87.0	325	20	87.0	13	2	B47415	mannose-1-phosphat
253	23	100.0	827	1	S56404	106	20	87.0	326	20	87.0	37	2	S48656	fusococcin recepto
254	23	100.0	827	1	C91273	107	20	87.0	327	20	87.0	42	2	T16667	hypothetical prote
255	23	100.0	827	2	C86114	108	20	87.0	328	20	87.0	50	2	A82759	hypothetical prote
256	23	100.0	831	2	J01655	109	20	87.0	329	20	87.0	54	4	AE0018	probable 6.1K prot
257	23	100.0	834	2	T03369	110	20	87.0	330	20	87.0	58	2	D95214	hypothetical prote
258	23	100.0	844	2	AD0047	111	20	87.0	331	20	87.0	58	2	D82759	hypothetical prote
259	23	100.0	858	2	T24062	112	20	87.0	332	20	87.0	58	2	C98078	hypothetical prote
260	23	100.0	865	2	B90644	113	20	87.0	333	20	87.0	68	2	JV0044	hypothetical 7.5K
261	23	100.0	865	2	B96558	114	20	87.0	334	20	87.0	71	2	S77822	hypothetical prote
262	23	100.0	865	2	B85495	115	20	87.0	335	20	87.0	82	2	AC2848	hypothetical prote
263	23	100.0	865	2	B64734	116	20	87.0	336	20	87.0	84	2	T33035	hypothetical prote
264	23	100.0	871	2	H81430	117	20	87.0	337	20	87.0	84	2	AE3321	hypothetical prote
265	23	100.0	876	2	B82163	118	20	87.0	338	20	87.0	88	2	C70911	hypothetical prote
266	23	100.0	883	1	RNBPT17	119	20	87.0	339	20	87.0	89	1	JN0685	calgranulin A - ra
267	23	100.0	884	1	RNBPT3	120	20	87.0	340	20	87.0	89	1	I56163	calgranulin A - mo
268	23	100.0	906	1	RNBPK1	121	20	87.0	341	20	87.0	91	2	C70891	hypothetical prote
269	23	100.0	916	2	I55441	122	20	87.0	342	20	87.0	104	2	B47062	pyocin transcripti
270	23	100.0	919	2	T16459	123	20	87.0	343	20	87.0	104	2	D95916	hypothetical prote
271	23	100.0	928	2	S40745	124	20	87.0	344	20	87.0	106	2	S72815	hypothetical prote
272	23	100.0	940	2	T01854	125	20	87.0	345	20	87.0	109	2	A86104	probable regulator
273	23	100.0	954	2	AF2756	126	20	87.0	346	20	87.0	111	2	T16516	hypothetical prote
274	23	100.0	954	2	E97537	127	20	87.0	347	20	87.0	112	2	B72741	hypothetical prote
275	23	100.0	966	1	QYIX1	128	20	87.0	348	20	87.0	117	2	T39528	very hypothetical
276	23	100.0	976	2	B87291	129	20	87.0	349	20	87.0	119	2	S38261	myohemerythrin - p
277	23	100.0	1010	2	G88554	130	20	87.0	350	20	87.0	122	2	F83167	hypothetical prote
278	23	100.0	1085	2	F70834	131	20	87.0	351	20	87.0	122	2	A95986	hypothetical expor
279	23	100.0	1111	2	G96693	132	20	87.0	352	20	87.0	123	2	AG1477	weakly inorganic p
280	23	100.0	1116	2	D97001	133	20	87.0	353	20	87.0	126	2	B82715	50S ribosomal prot
281	23	100.0	1134	2	S53955	134	20	87.0	354	20	87.0	126	2	T21762	hypothetical prote
282	23	100.0	1157	2	T43258	135	20	87.0	355	20	87.0	127	2	B84448	hypothetical prote
283	23	100.0	1157	2	T43259	136	20	87.0	356	20	87.0	127	2	B97097	hypothetical prote
284	23	100.0	1158	2	T25082	137	20	87.0	357	20	87.0	129	1	HSCH2A	histone H2A - chic
285	23	100.0	1165	2	S58236	138	20	87.0	358	20	87.0	129	2	I50457	hypothetical prote
286	23	100.0	1256	2	G97902	139	20	87.0	359	20	87.0	130	2	F84249	hypothetical prote
287	23	100.0	1257	2	T09493	140	20	87.0	360	20	87.0	134	2	I51233	prolactin - Japane
288	23	100.0	1257	2	T13957	141	20	87.0	361	20	87.0	137	2	T20957	hypothetical prote
289	23	100.0	1280	2	E95031	142	20	87.0	362	20	87.0	138	2	AE0386	N utilization subs
290	23	100.0	1292	2	A88225	143	20	87.0	363	20	87.0	138	2	T46133	hypothetical prote
291	23	100.0	1292	2	T24559	144	20	87.0	364	20	87.0	138	2	AF2447	hypothetical prote
292	23	100.0	1445	2	A59437	145	20	87.0	365	20	87.0	139	1	FJECB	transcription term
293	23	100.0	1449	2	T20181	146	20	87.0	366	20	87.0	139	2	E90687	transcription term
294	23	100.0	1462	2	T11648	147	20	87.0	367	20	87.0	139	2	A85538	transcription term
295	23	100.0	1465	2	S31262	148	20	87.0	368	20	87.0	139	2	AB0554	N utilization subs
296	23	100.0	1467	2	PC1253	149	20	87.0	369	20	87.0	141	2	D91263	probable phn opo
297	23	100.0	1508	2	E87696	150	20	87.0	370	20	87.0	142	2	H69825	hypothetical prote
298	23	100.0	1526	2	T13823	151	20	87.0	371	20	87.0	143	2	H84983	N utilization subs
299	23	100.0	1584	2	T20180	152	20	87.0	372	20	87.0	144	2	G35719	phnO protein - Esc
300	23	100.0	1586	2	T20179	153	20	87.0	373	20	87.0	145	2	C71378	hypothetical prote
301	23	100.0	1607	2	T43212	154	20	87.0	374	20	87.0	148	2	T13224	hypothetical prote
302	23	100.0	1628	2	E90538	155	20	87.0	375	20	87.0	148	2	H95849	hypothetical prote
303	23	100.0	1697	2	T00079	156	20	87.0	376	20	87.0	150	2	T36600	hypothetical prote
304	23	100.0	1750	2	E86151	157	20	87.0	377	20	87.0	151	2	S58022	ribosomal protein
305	23	100.0	1756	2	T02599	158	20	87.0	378	20	87.0	151	2	E83170	hypothetical prote
306	23	100.0	1778	2	T50074	159	20	87.0	379	20	87.0	153	2	A71638	hypothetical prote
307	23	100.0	1802	2	S52611	160	20	87.0	380	20	87.0	154	2	AG1021	probable acetyltra
308	23	100.0	1803	2	S56894	161	20	87.0	381	20	87.0	156	2	B82098	N utilization subs
309	23	100.0	1956	2	T00051	162	20	87.0	382	20	87.0	157	2	S41891	tryptophan 2-monoo
310	23	100.0	2061	2	T13751	163	20	87.0	383	20	87.0	157	2	AF2739	acetyltransferase
311	23	100.0	2061	2	A84669	164	20	87.0	384	20	87.0	157	2	D97520	hypothetical prote
312	23	100.0	2168	2	D88131	165	20	87.0	385	20	87.0	157	2	T37041	hypothetical prote
313	23	100.0	2215	2	T00348	166	20	87.0	386	20	87.0	158	2	AH1985	hypothetical prote
314	23	100.0	2437	2	S53611	167	20	87.0	387	20	87.0	161	2	F75542	conserved hypotet
315	23	100.0	2559	2	T09144	168	20	87.0	388	20	87.0	162	2	T30284	cytochrome P-450 h
316	23	100.0	2670	2	A46719	169	20	87.0	389	20	87.0	162	2	D84314	hypothetical prote
317	23	100.0	2671	2	A49873	170	20	87.0	390	20	87.0	163	2	B82373	hypothetical prote
318	23	100.0	3079	1	RGBY12	171	20	87.0	391	20	87.0	166	2	F84443	hypothetical prote
319	23	100.0	3084	1	MMWSA	172	20	87.0	392	20	87.0	166	2	H96940	hypothetical prote
320	23	100.0	3225	2	D81702	173	20	87.0	393	20	87.0	170	2	AF1453	antigen A (import
321	23	100.0	3268	2	S69625	174	20	87.0	394	20	87.0	170	2	H69850	mutator MutT prote

395	20	87.0	170	2	T34588	hypothetical prote	468	20	87.0	229	2	A60972	prolactin precursor
396	20	87.0	172	2	T25066	hypothetical prote	469	20	87.0	229	2	JC4631	prolactin precursor
397	20	87.0	174	2	H83481	hypothetical prote	470	20	87.0	229	2	B37944	CAMP response elem
398	20	87.0	175	2	S18882	prolactin - Americ	471	20	87.0	229	2	A37944	CAMP response elem
399	20	87.0	176	2	A06684	bacteriophage host	472	20	87.0	229	2	A69971	conserved hypotet
400	20	87.0	177	2	A28106	prolactin, 20K - M	473	20	87.0	229	2	A89473	protein F52D2.2 [i
401	20	87.0	182	2	S75533	hydrogenase small	474	20	87.0	233	2	T20671	hypothetical prote
402	20	87.0	187	2	S06677	prolactin II - chu	475	20	87.0	234	2	G97225	diverged arginase
403	20	87.0	187	2	S02304	prolactin I - chum	476	20	87.0	235	2	S73536	uridylylate kinase p
404	20	87.0	188	2	B28106	prolactin, 24K - M	477	20	87.0	235	2	C87687	acyltransferase fa
405	20	87.0	190	2	T26609	hypothetical prote	478	20	87.0	236	2	G69054	conserved hypotet
406	20	87.0	192	2	A10268	anthranilate synth	479	20	87.0	237	2	A45929	spectrin beta chai
407	20	87.0	192	2	S59537	heat shock transcr	480	20	87.0	237	2	S36343	opacity protein op
408	20	87.0	192	2	T06284	hypothetical prote	481	20	87.0	238	2	HHEF67	heat shock protein
409	20	87.0	196	2	D84178	50S ribosomal prot	482	20	87.0	238	2	D83847	two-component resp
410	20	87.0	196	2	B83226	aliphatic amidase	483	20	87.0	239	2	E86346	two-component resp
411	20	87.0	196	2	S03884	regulatory protein	484	20	87.0	240	1	G69691	hypothetical prote
412	20	87.0	198	1	A06620	prolactin - green	485	20	87.0	240	2	T14978	hypothetical prote
413	20	87.0	199	1	LC80	prolactin - horse	486	20	87.0	241	2	D89928	hypothetical prote
414	20	87.0	199	2	PN0128	prolactin - sei wh	487	20	87.0	241	2	A64155	hypothetical prote
415	20	87.0	199	2	JS0430	prolactin - elepha	488	20	87.0	241	2	T39231	probable lysophosp
416	20	87.0	199	2	S15131	prolactin - Arabia	489	20	87.0	242	2	AD2982	transcription regu
417	20	87.0	199	2	A71411	proteasome endopep	490	20	87.0	242	2	D98301	uxu operon regulat
418	20	87.0	200	2	AC0369	cytochrome C-type	491	20	87.0	242	2	AH2794	polyketide biosynt
419	20	87.0	200	2	B32477	prolactin II precu	492	20	87.0	242	2	G97573	frne protein VCA01
420	20	87.0	204	2	T51982	proteasome endopep	493	20	87.0	242	2	H69471	conserved hypotet
421	20	87.0	207	2	A60969	prolactin precursor	494	20	87.0	245	2	H90196	hypothetical prote
422	20	87.0	207	2	S21965	prolactin - silver	495	20	87.0	245	2	B95933	conserved hypotet
423	20	87.0	207	2	T29181	hypothetical prote	496	20	87.0	246	2	T35927	conserved hypotet
424	20	87.0	208	2	T26144	hypothetical prote	497	20	87.0	250	2	S67449	probable endonucle
425	20	87.0	209	2	S30541	prolactin precursor	498	20	87.0	252	2	VHUUU	nucleocapsid prote
426	20	87.0	209	2	G71430	hypothetical prote	499	20	87.0	254	1	A64175	molybdate-binding
427	20	87.0	210	1	S01435	prolactin precursor	500	20	87.0	254	2	T05076	hypothetical prote
428	20	87.0	210	2	S15084	prolactin precursor	501	20	87.0	255	2	S04668	hypothetical prote
429	20	87.0	210	2	PN0092	prolactin precursor	502	20	87.0	255	2	C70750	hypothetical prote
430	20	87.0	210	2	S16765	prolactin precursor	503	20	87.0	255	2	D86693	conserved hypotet
431	20	87.0	210	2	A31364	prolactin precursor	504	20	87.0	256	2	S51050	hypothetical prote
432	20	87.0	210	2	S34351	prolactin precursor	505	20	87.0	257	1	C64812	molybdate-binding
433	20	87.0	210	2	S52475	prolactin - Atlant	506	20	87.0	257	2	G90727	molybdate-binding
434	20	87.0	210	2	S71486	prolactin precursor	507	20	87.0	257	2	H85578	molybdate-binding
435	20	87.0	210	2	D84273	fibrillarlin limpor	508	20	87.0	257	2	AC0595	molybdate-binding
436	20	87.0	210	2	AH2668	ABC transporter, m	509	20	87.0	257	2	AC1879	hypothetical prote
437	20	87.0	210	2	F97450	hypothetical prote	510	20	87.0	257	2	T29183	hypothetical prote
438	20	87.0	211	2	S00359	prolactin precursor	511	20	87.0	258	2	S16612	opacity protein op
439	20	87.0	211	2	H86852	hypothetical prote	512	20	87.0	258	2	F69479	nicotinate-nucleot
440	20	87.0	212	2	S151275	prolactin precursor	513	20	87.0	258	2	T05194	hypothetical prote
441	20	87.0	212	2	A32477	prolactin I precu	514	20	87.0	259	2	G75400	probable oxidoredu
442	20	87.0	212	2	S15034	prolactin-I - Moza	515	20	87.0	259	2	S41890	hypothetical prote
443	20	87.0	212	2	C70737	probable sigp prot	516	20	87.0	260	2	S16611	opacity protein op
444	20	87.0	213	2	T02697	hypothetical prote	517	20	87.0	260	2	T42960	hypothetical prote
445	20	87.0	215	2	C86818	hypothetical prote	518	20	87.0	261	2	AE3499	O-sialoglycoprotei
446	20	87.0	215	2	S18228	replication initia	519	20	87.0	261	2	AG3116	conserved hypotet
447	20	87.0	216	2	F71002	hypothetical prote	520	20	87.0	261	2	G69117	diphosphate hydrolase
448	20	87.0	216	2	G75128	hypothetical prote	521	20	87.0	265	2	T35850	probable synthase
449	20	87.0	217	2	C37944	CAMP response elem	522	20	87.0	265	2	T33852	hypothetical prote
450	20	87.0	217	2	D96013	probable partial t	523	20	87.0	265	2	F98170	hypothetical prote
451	20	87.0	220	2	A95339	hypothetical prote	524	20	87.0	266	2	A48349	U128 protein - ate
452	20	87.0	220	2	T09108	RNA binding protei	525	20	87.0	266	2	D95373	hypothetical prote
453	20	87.0	220	2	S26685	CAMP response elem	526	20	87.0	267	2	T22502	hypothetical prote
454	20	87.0	221	2	A45181	Max-binding bHLH-Z	527	20	87.0	268	2	D86270	F21F33.14 protein
455	20	87.0	223	2	AF1345	hypothetical prote	528	20	87.0	268	2	B47112	growth response pr
456	20	87.0	223	2	A11715	hypothetical prote	529	20	87.0	269	2	AG490	TCR V beta CRE-mot
457	20	87.0	224	2	S20463	siderophore biosyn	530	20	87.0	270	2	AG0916	probable hydrolase
458	20	87.0	224	2	I39875	siderophore biosyn	531	20	87.0	271	2	S12560	transcription fact
459	20	87.0	224	2	AI3595	frnE protein limpo	532	20	87.0	272	2	S59042	splicing factor SR
460	20	87.0	226	1	LCRT	prolactin precursor	533	20	87.0	272	2	G89758	conserved hypotet
461	20	87.0	226	2	A49159	prolactin - golden	534	20	87.0	277	2	G71849	amino acid ABC tra
462	20	87.0	227	1	LC8U	prolactin precursor	535	20	87.0	277	2	D64666	glutamine ABC tran
463	20	87.0	228	1	LCMS	prolactin precursor	536	20	87.0	278	2	JE0216	28k surface anti
464	20	87.0	228	2	A61402	prolactin precursor	537	20	87.0	278	2	D70504	hypothetical prote
465	20	87.0	228	2	F97323	protein-disulfide	538	20	87.0	278	2	S36101	CAMP response elem
466	20	87.0	229	1	LCPG	prolactin precursor	539	20	87.0	279	2	A87360	hypothetical prote
467	20	87.0	229	2	A61133	prolactin precursor	540	20	87.0	280	1	A53419	2,3-dihydroxy-4-ph

541	20	87.0	280	2	H81237	phn0-related prote	614	20	87.0	336	2	S74462	hypothetical prote
542	20	87.0	280	2	F82010	hypothetical prote	615	20	87.0	336	2	B6463	AIgi-like protein,
543	20	87.0	281	2	T28857	hypothetical prote	616	20	87.0	338	2	E95244	glycerol-3-phospha
544	20	87.0	283	2	D98325	hypothetical prote	617	20	87.0	338	2	C98109	glycerol-3-phospha
545	20	87.0	284	2	F71613	hypothetical prote	618	20	87.0	339	2	T25142	hypothetical prote
546	20	87.0	284	2	AF0695	probable secreted	619	20	87.0	339	2	T25204	hypothetical prote
547	20	87.0	285	2	H85356	hypothetical prote	620	20	87.0	341	2	H96499	probable fructose
548	20	87.0	287	2	JE0220	28k surface antige	621	20	87.0	341	2	E90814	beta-N-acetylgluco
549	20	87.0	289	2	T08176	glucose-1-phosphat	622	20	87.0	341	2	S20827	CAMP response elem
550	20	87.0	290	2	S41555	TyA protein - years	623	20	87.0	341	2	S26686	beta-N-acetylgluco
551	20	87.0	290	2	S63841	TyA protein - years	624	20	87.0	341	2	A85674	protein T27A10.7 l
552	20	87.0	292	2	B70721	hypothetical prote	625	20	87.0	341	2	H89500	probable glucosida
553	20	87.0	293	2	T31480	hypothetical prote	626	20	87.0	341	2	H64854	probable glycosyl
554	20	87.0	295	2	C82558	bifunctional methy	627	20	87.0	341	2	AB0644	glycoprotein endop
555	20	87.0	296	2	G97059	era GTFase [import	628	20	87.0	343	2	D83718	probable portal pr
556	20	87.0	296	2	C81906	hypothetical prote	629	20	87.0	344	2	S22796	CAMP response elem
557	20	87.0	296	2	G81111	conserved hypothet	630	20	87.0	344	2	UC5601	CAMP response elem
558	20	87.0	296	2	D82515	ketoreductase XF27	631	20	87.0	344	2	JC5602	probable asd prote
559	20	87.0	298	2	F69119	cation efflux syst	632	20	87.0	345	2	E70794	probable heat choc
560	20	87.0	299	2	A95293	TRM17a probable tr	633	20	87.0	345	2	T02609	anthranilate phosp
561	20	87.0	300	1	TVVZVW	protein kinase (EC	634	20	87.0	348	1	D24723	probable quinone o
562	20	87.0	300	1	TVVZ92	protein kinase (EC	635	20	87.0	348	2	F97459	oxidoreductase hom
563	20	87.0	300	1	A36855	protein kinase (EC	636	20	87.0	349	2	AB1715	oxidoreductase hom
564	20	87.0	300	2	H72171	H1R protein - vari	637	20	87.0	349	2	AG1344	centromere-binding
565	20	87.0	300	2	T28600	hypothetical prote	638	20	87.0	351	1	JSBYPI	heat shock transcr
566	20	87.0	302	2	T37440	protein kinase - v	639	20	87.0	351	2	S25480	hypothetical prote
567	20	87.0	302	2	B35961	hypothetical 21k p	640	20	87.0	351	2	E87317	hypothetical prote
568	20	87.0	302	2	S69725	hypothetical prote	641	20	87.0	351	2	T01845	hypothetical prote
569	20	87.0	303	2	A49053	glucose-1-phosphat	642	20	87.0	353	2	D97295	probable pksII pro
570	20	87.0	303	2	A69542	conserved hypothet	643	20	87.0	353	2	T72958	parvulin-like pept
571	20	87.0	304	2	D81815	hypothetical DNA-b	644	20	87.0	356	2	T19792	hypothetical prote
572	20	87.0	304	2	T16704	hypothetical prote	645	20	87.0	357	2	S35250	flagellar biosynth
573	20	87.0	305	2	A72636	hypothetical prote	646	20	87.0	357	2	QJ1292	hypothetical 39K p
574	20	87.0	307	2	B83167	hypothetical prote	647	20	87.0	358	2	A70746	hypothetical prote
575	20	87.0	308	1	A34082	branched-chain-ami	648	20	87.0	358	2	T17619	hypothetical prote
576	20	87.0	308	2	I48080	coatomer complex e	649	20	87.0	359	2	A96534	hypothetical prote
577	20	87.0	308	2	I46019	coatomer complex e	650	20	87.0	359	2	B72359	lipopolysaccharide
578	20	87.0	308	2	T40266	probable ras relat	651	20	87.0	360	2	D71323	conserved hypothet
579	20	87.0	309	1	XNECV	branched-chain-ami	652	20	87.0	360	2	H95401	probable LacI-fami
580	20	87.0	309	2	H91216	branched-chain-ami	653	20	87.0	360	2	H95401	gibberellin 20-dio
581	20	87.0	309	2	A86063	branched-chain ami	654	20	87.0	361	2	T06330	methylethyl-DNA-[pr
582	20	87.0	309	2	AD0924	branched-chain ami	655	20	87.0	361	2	AH3446	probable 3-dehydro
583	20	87.0	309	2	T18579	cyclophilin isoform	656	20	87.0	361	2	F86973	splicing factor-1i
584	20	87.0	311	2	H69394	cysteine synthase	657	20	87.0	361	2	T42525	3-dehydroquinatase
585	20	87.0	312	2	G84058	cysteine synthase	658	20	87.0	362	1	S17768	adenylate cyclase
586	20	87.0	312	2	T35742	hypothetical prote	659	20	87.0	363	2	S60684	hypothetical prote
587	20	87.0	313	2	AH3058	2-HYDROXY-3-OXOPRO	660	20	87.0	363	2	B83023	hypothetical prote
588	20	87.0	313	2	H98227	3-hydroxyisobutyra	661	20	87.0	364	1	PAQXF	fructose-bisphosph
589	20	87.0	315	2	H84938	flagellar motor sw	662	20	87.0	364	2	B87124	conserved hypothet
590	20	87.0	315	2	T50561	SINAI protein [imp	663	20	87.0	364	2	T34713	hypothetical prote
591	20	87.0	315	2	H96598	protein P20N2.8 [l	664	20	87.0	365	2	T06991	gibberellin 20-dio
592	20	87.0	315	2	B82229	hypothetical prote	665	20	87.0	365	2	T06990	gibberellin 20-dio
593	20	87.0	316	2	T01771	hypothetical prote	666	20	87.0	365	2	G83373	hypothetical prote
594	20	87.0	317	1	JC4827	protein kinase (EC	667	20	87.0	365	2	T37730	probable pre-mRNA
595	20	87.0	317	2	A13535	penicillin amidase	668	20	87.0	365	2	A71410	hypothetical prote
596	20	87.0	317	2	S54548	hypothetical prote	669	20	87.0	367	2	S72924	hypothetical prote
597	20	87.0	318	2	S37648	hypothetical prote	670	20	87.0	369	2	F84229	probable peptidase
598	20	87.0	321	2	G71468	probable fa/phosph	671	20	87.0	369	2	F81178	histone deacetylase
599	20	87.0	321	2	T31847	conserved hypothet	672	20	87.0	369	2	H75461	sensor histidine k
600	20	87.0	322	2	D72737	aspartate-semialde	673	20	87.0	370	2	G87212	conserved hypothet
601	20	87.0	323	2	S42426	ABC transporter, A	674	20	87.0	370	2	I38177	ras-related GTPase
602	20	87.0	325	2	E75404	probable NADPH2:qu	675	20	87.0	374	2	AC3569	glucuronate isomer
603	20	87.0	326	2	E95941	quinone oxidoreduc	676	20	87.0	375	2	T32251	hypothetical prote
604	20	87.0	327	2	A12677	beta-glucosidase (	677	20	87.0	375	2	AB0959	hypothetical prote
605	20	87.0	327	2	F97835	hypothetical prote	678	20	87.0	381	2	G83518	probable acyl-CoA
606	20	87.0	328	2	C70745	hypothetical prote	679	20	87.0	381	2	B82840	conserved hypothet
607	20	87.0	329	2	B84199	hypothetical prote	680	20	87.0	382	2	F87464	hypothetical prote
608	20	87.0	330	2	H70500	probable moxR prot	681	20	87.0	383	2	T22752	hypothetical prote
609	20	87.0	331	1	C69026	acetylpolymine am	682	20	87.0	385	2	G84459	probable GDP-manno
610	20	87.0	332	2	D70605	probable rhoA prot	683	20	87.0	385	2	A19266	hypothetical prote
611	20	87.0	333	2	H89961	hypothetical prote	684	20	87.0	386	2	T26108	hypothetical prote
612	20	87.0	334	2	T33201	hypothetical prote	685	20	87.0	389	2	E86634	hypothetical prote
613	20	87.0	335	2	G96607	probable galactino	686	20	87.0	391	2	G84278	X-pro aminopeptida



687	20	87.0	396	2	S56496	prophage P4 integr	760	20	87.0	482	2	B83113	catalase PA4236 [i
688	20	87.0	397	2	B70048	conserved hypotet	761	20	87.0	482	2	A83655	lysine decarboxyla
689	20	87.0	398	1	S47520	vitamin D-3 25-hyd	762	20	87.0	483	2	S37055	catalase (EC 1.11.
690	20	87.0	398	1	XUECGA	glycine C-acetyltr	763	20	87.0	483	2	JH0532	catalase (EC 1.11.
691	20	87.0	398	2	G91190	2-amino-3-ketobuty	764	20	87.0	484	2	A58663	catalase (EC 1.11.
692	20	87.0	398	2	H86037	glycine C-acetyltr	765	20	87.0	485	2	A70706	probable phoR prot
693	20	87.0	398	2	A10973	glycine C-acetyltr	766	20	87.0	485	2	S73333	MG260 homolog - My
694	20	87.0	400	2	S76929	hypothetical prote	767	20	87.0	487	2	T34858	catalase (EC 1.11.
695	20	87.0	400	2	A97535	ispD/ispF bifuncti	768	20	87.0	489	1	VGXPMV	surface glycoprote
696	20	87.0	400	2	AC2754	ISPD/ISPF bifuncti	769	20	87.0	489	1	C72317	conserved hypotet
697	20	87.0	403	2	B35401	cytochrome P450 10	770	20	87.0	490	2	E69114	conserved hypotet
698	20	87.0	403	2	S02856	site-specific DNA-	771	20	87.0	492	1	E69114	conserved hypotet
699	20	87.0	404	2	AC2754	3-oxoacyl-[acyl-ca	772	20	87.0	492	2	S32491	conserved hypotet
700	20	87.0	404	2	AC2754	3-oxoacyl-[acyl-ca	773	20	87.0	494	2	B89870	testosterone 7alph
701	20	87.0	404	2	AC2754	starvation-sensing	774	20	87.0	494	2	H82489	hypothetical prote
702	20	87.0	404	2	AC2754	starvation-sensing	775	20	87.0	494	2	H82489	conserved hypotet
703	20	87.0	405	2	G95903	hypothetical prote	776	20	87.0	499	2	A55227	hypothetical prote
704	20	87.0	406	1	SVECA1	3-oxoacyl-[acyl-ca	777	20	87.0	500	2	T24901	catalase (EC 1.11.
705	20	87.0	406	2	G91029	3-oxoacyl-[acyl-ca	778	20	87.0	501	2	A29487	hypothetical prote
706	20	87.0	406	2	H85873	3-oxoacyl-[acyl-ca	779	20	87.0	501	2	A34236	cytochrome P450 3A
707	20	87.0	406	2	T28957	hypothetical prote	780	20	87.0	503	2	JC4702	cytochrome P450 3A
708	20	87.0	406	2	S72894	exopolysphatase	781	20	87.0	503	2	H71659	transcription term
709	20	87.0	406	2	AF2521	transposase alr735	782	20	87.0	504	2	A29410	cytochrome P450, g
710	20	87.0	406	2	AT12515	transposase alr730	783	20	87.0	504	2	SS0892	cytochrome P450 3A
711	20	87.0	409	2	T11743	pr47 protein - pig	784	20	87.0	507	2	AD3621	catalase (EC 1.11.
712	20	87.0	413	2	JC8001	N-acetylglactosam	785	20	87.0	514	2	A45228	25-hydroxyvitamin
713	20	87.0	415	2	JC71167	C kinase 1 interac	786	20	87.0	514	2	C36901	chorion transcript
714	20	87.0	415	2	C70552	hypothetical prote	787	20	87.0	515	1	CSBYP	catalase (EC 1.11.
715	20	87.0	415	2	B83634	hypothetical prote	788	20	87.0	515	2	AE0186	probable decarboxy
716	20	87.0	416	2	T51096	thyroid hormone re	789	20	87.0	522	2	AB2928	hypothetical prote
717	20	87.0	416	2	A56486	perinuclear bindin	790	20	87.0	522	2	E98354	hypothetical prote
718	20	87.0	421	2	B82062	conserved hypotet	791	20	87.0	523	2	C70717	aliqui (AB011415) l
719	20	87.0	421	2	B71463	probable im protei	792	20	87.0	523	2	G96809	probable purH prot
720	20	87.0	422	1	JC12110	polyketide beta-ke	793	20	87.0	523	2	G96777	protein F28K19.28
721	20	87.0	422	2	T24775	hypothetical prote	794	20	87.0	526	1	TVFVR	hypothetical prote
722	20	87.0	427	2	A84820	hypothetical prote	795	20	87.0	526	1	OKFVVR	protein-tyrosine k
723	20	87.0	428	2	S76184	hypothetical prote	796	20	87.0	526	2	S15582	protein-tyrosine k
724	20	87.0	429	2	AD1921	hypothetical prote	797	20	87.0	526	2	S20808	protein-tyrosine k
725	20	87.0	430	2	B87097	probable conserved	798	20	87.0	526	2	S26420	protein-tyrosine k
726	20	87.0	430	2	C86346	FlaF4.3 protein -	799	20	87.0	526	2	T39748	probable ser/thr p
727	20	87.0	431	2	T11854	protein kinase (EC	800	20	87.0	527	2	D96014	probable sugar upt
728	20	87.0	431	2	F84332	succinoglycan bios	801	20	87.0	527	2	T45439	probable phosphori
729	20	87.0	435	2	T24477	hypothetical prote	802	20	87.0	531	2	T35226	rharnogalacturonas
730	20	87.0	435	2	S07040	hypothetical prote	803	20	87.0	531	2	B84492	nitrate reductase
731	20	87.0	437	2	T26767	alpha-amylase (EC	804	20	87.0	534	2	S57974	probable retroelem
732	20	87.0	437	2	T26767	hypothetical prote	805	20	87.0	534	2	F84398	hypothetical prote
733	20	87.0	438	1	ALBH	alpha-amylase (EC	806	20	87.0	538	2	A54391	phosphate ABC tran
734	20	87.0	440	2	JC2532	secretin receptor	807	20	87.0	538	2	T29835	translation initia
735	20	87.0	440	2	A82369	thiamin-phosphate	808	20	87.0	542	2	T29835	sphingosine-1-phos
736	20	87.0	444	2	TS0931	alpha-amylase (EC	809	20	87.0	546	2	T48520	hypothetical prote
737	20	87.0	444	2	B83249	conserved hypotet	810	20	87.0	547	2	A40656	hypothetical prote
738	20	87.0	444	2	T27863	hypothetical prote	811	20	87.0	547	2	AE1022	probable membrane
739	20	87.0	445	2	S19990	alpha-amylase (EC	812	20	87.0	549	2	C72387	hypothetical prote
740	20	87.0	446	2	B82975	conserved hypotet	813	20	87.0	554	2	T15992	hypothetical prote
741	20	87.0	448	2	A69959	glycine dehydrogen	814	20	87.0	556	2	C89181	hypothetical prote
742	20	87.0	448	2	H83335	probable MFS trans	815	20	87.0	557	2	AD2832	DNA repair protein
743	20	87.0	448	2	S57686	hypothetical prote	816	20	87.0	557	2	H97609	DNA repair protein
744	20	87.0	451	2	F84492	hypothetical prote	817	20	87.0	557	2	S56342	yidB protein - Esc
745	20	87.0	451	2	A36908	probable Athila re	818	20	87.0	557	2	H91265	hypothetical prote
746	20	87.0	452	2	JC4038	spore cortex penic	819	20	87.0	562	2	E86106	yidB protein [simi
747	20	87.0	452	2	F89720	47K glycoprotein p	820	20	87.0	562	2	T05758	hypothetical prote
748	20	87.0	458	2	T27217	protein R1010.2 l	821	20	87.0	567	2	F82384	hypothetical prote
749	20	87.0	460	2	C96736	hypothetical prote	822	20	87.0	571	2	T26638	probable phosphoma
750	20	87.0	462	2	H82152	probable ketoacyl-	823	20	87.0	573	2	A41319	hypothetical prote
751	20	87.0	467	2	H82152	PTS system, fructo	824	20	87.0	573	2	C64611	3-oxosteroide 1-deh
752	20	87.0	469	2	B95958	probable glucurona	825	20	87.0	574	2	T14162	hypothetical prote
753	20	87.0	471	2	T34956	probable UDP-N-ace	826	20	87.0	575	2	S59740	hABC transport pro
754	20	87.0	472	2	AE1955	two-component sens	827	20	87.0	575	2	T45668	NMD protein - yea
755	20	87.0	473	2	D96591	hypothetical prote	828	20	87.0	575	2	S62713	hypothetical prote
756	20	87.0	476	2	B71696	probable transport	829	20	87.0	578	2	S51379	phytochrome la - M
757	20	87.0	480	1	B70804	DNA repair protein	830	20	87.0	580	2	T34668	pyruvate phosphoe
758	20	87.0	480	2	JC7672	catalase (EC 1.11.	831	20	87.0	581	1	RYERT	pyruvate dehydroge
759	20	87.0	481	2	T28900	hypothetical prote	832	20	87.0	583	2	S17671	DNA primase (EC 2.
	20	87.0	482	2	S49465	catalase (EC 1.11.		20	87.0	585	2	S15963	protein-tyrosine-p
	20	87.0						20	87.0				hypothetical prote



833	20	87.0	586	1	ORXLE	estrogen receptor	906	20	87.0	693	1	TNBEF7	73.8K alpha trans-
834	20	87.0	586	2	B84271	glutamyl-tRNA synt	907	20	87.0	694	2	T30725	probable abortive
835	20	87.0	586	2	T39769	trp-asp repeats co	908	20	87.0	698	2	T32840	hypothetical prote
836	20	87.0	586	2	AD2493	hypothetical prote	909	20	87.0	699	2	C96655	hypothetical prote
837	20	87.0	589	1	QRCH	estrogen receptor	910	20	87.0	701	2	S64737	80K estrogen recep
838	20	87.0	590	2	B85010	hypothetical prote	911	20	87.0	706	1	WZBED8	gene 45 protein -
839	20	87.0	590	2	S63193	hypothetical prote	912	20	87.0	712	2	AB2776	DNA gyrase subunit b
840	20	87.0	591	2	C84220	propionyl-CoA carb	913	20	87.0	712	2	H97555	DNA gyrase chain b
841	20	87.0	592	2	S43570	COSB5.6 protein (c	914	20	87.0	719	1	MNKR3D	nonstructural prot
842	20	87.0	595	1	QRHUE	estrogen receptor	915	20	87.0	721	2	F82198	probable toxin sec
843	20	87.0	595	1	AD1710	estrogen receptor	916	20	87.0	723	1	S30105	tryptophan 2-monoo
844	20	87.0	599	1	QRMSE	estradiol receptor	917	20	87.0	724	2	C49423	semaphorin II prec
845	20	87.0	599	2	AG1964	estrogen receptor	918	20	87.0	724	2	D85075	probable athila tr
846	20	87.0	600	1	QRRT	hypothetical prote	919	20	87.0	728	2	S55601	hypothetical prote
847	20	87.0	601	2	A28577	estrogen receptor	920	20	87.0	730	2	AI3480	penicillin-binding
848	20	87.0	601	2	D96001	NADPH-ferrihemopro	921	20	87.0	733	2	S78376	photosystem I P700
849	20	87.0	601	2	T00119	probable 1,4-alpha	922	20	87.0	733	2	F84476	probable Ahila re
850	20	87.0	602	2	T45386	probable transcrip	923	20	87.0	734	2	C69691	GRP pyrophosphokin
851	20	87.0	604	2	C57784	endopeptidase IV [	924	20	87.0	734	2	S73206	photosystem I prot
852	20	87.0	604	2	S25203	MTG8 protein splic	925	20	87.0	735	2	G02937	feritin beta - cr
853	20	87.0	606	2	T13152	srMR protein - Str	926	20	87.0	738	2	AC1265	(p)ppGpp synthetas
854	20	87.0	609	2	S28283	WDR1 protein - hum	927	20	87.0	738	2	AE1627	(p)ppGpp synthetas
855	20	87.0	610	2	T16194	hypothetical prote	928	20	87.0	749	2	I39708	tryptophan 2-monoo
856	20	87.0	614	1	S43237	hypothetical prote	929	20	87.0	752	4	AS7784	tryptophan 2-monoo
857	20	87.0	617	2	T29660	2-methyleneglutar	930	20	87.0	754	2	S60464	mes-3 protein - Ca
858	20	87.0	618	2	S11445	hypothetical prote	931	20	87.0	754	2	G87767	protein mes-3 [imp
859	20	87.0	619	2	D90072	parasporal crystal	932	20	87.0	755	1	DAAGWT	tryptophan 2-monoo
860	20	87.0	620	2	T10423	hypothetical prote	933	20	87.0	755	1	QAGAT	tryptophan 2-monoo
861	20	87.0	620	2	E84481	estrogen receptor	934	20	87.0	755	2	AI3228	tryptophan 2-monoo
862	20	87.0	623	2	G70644	probable protein k	935	20	87.0	758	2	E83884	hypothetical prote
863	20	87.0	623	2	A48315	probable spA prot	936	20	87.0	759	2	AE1314	hypothetical prote
864	20	87.0	625	2	H70330	lamin III - Africa	937	20	87.0	759	2	AE1686	pyruvate formate-1
865	20	87.0	625	2	T20634	hypothetical prote	938	20	87.0	761	2	S46611	pyruvate formate-1
866	20	87.0	629	2	T06675	hypothetical prote	939	20	87.0	763	2	A88881	YTA10 protein - ye
867	20	87.0	630	2	F85074	hypothetical prote	940	20	87.0	765	1	ISHUT1	hypothetical prote
868	20	87.0	634	2	T27881	hypothetical prote	941	20	87.0	767	1	WMBEP6	DNA topoisomerase
869	20	87.0	638	2	T20944	hypothetical prote	942	20	87.0	767	2	JU0144	ribonucleoside-dip
870	20	87.0	639	2	C83624	probable two-compo	943	20	87.0	767	2	A49546	DNA topoisomerase
871	20	87.0	639	2	T43190	probable actin-bin	944	20	87.0	768	2	A82009	DNA topoisomerase
872	20	87.0	639	2	AI2663	potassium uptake p	945	20	87.0	768	2	H81236	DNA topoisomerase
873	20	87.0	639	2	H97445	potassium uptake p	946	20	87.0	770	1	WZBE30	gene 30 protein -
874	20	87.0	640	2	S52047	deoxyribodipyrimid	947	20	87.0	772	2	A48822	protein-glutamine
875	20	87.0	644	2	B71515	probable tail-spec	948	20	87.0	775	2	T38352	hypothetical prote
876	20	87.0	645	2	T27186	hypothetical prote	949	20	87.0	776	2	T15411	hypothetical prote
877	20	87.0	648	2	F82290	soluble lytic mure	950	20	87.0	780	1	WMBEH8	infected cell prot
878	20	87.0	649	2	T01106	hypothetical prote	951	20	87.0	782	2	E90427	hypothetical prote
879	20	87.0	649	2	B81673	tail specific prot	952	20	87.0	783	2	T00782	probable anthranil
880	20	87.0	650	2	S64939	CDC45 protein - ye	953	20	87.0	785	1	WMBEK8	infected cell prot
881	20	87.0	652	2	T20131	proprotein convert	954	20	87.0	785	1	WMBEW8	infected cell prot
882	20	87.0	652	2	T10576	hypothetical prote	955	20	87.0	786	2	E87565	conserved hypotet
883	20	87.0	655	2	T16538	hypothetical prote	956	20	87.0	786	2	T33856	hypothetical prote
884	20	87.0	656	2	D82388	hypothetical prote	957	20	87.0	788	2	B84857	hypothetical prote
885	20	87.0	657	2	T49875	glycogen operon pr	958	20	87.0	792	2	A70476	ATP-dependent DNA
886	20	87.0	660	2	S03383	probable amidase -	959	20	87.0	792	2	AH3619	transketolase (EC
887	20	87.0	662	2	G95929	gamma-glutamyltran	960	20	87.0	796	2	T34805	hypothetical prote
888	20	87.0	664	1	TNBE70	probable methylcro	961	20	87.0	802	2	C86303	probable vacuolar
889	20	87.0	668	2	AC1337	70.5K alpha trans-	962	20	87.0	803	1	RGBYW6	hypothetical prote
890	20	87.0	668	2	AC1377	transcription anti	963	20	87.0	803	1	H87197	regulatory protein
891	20	87.0	668	2	AC1377	transcription anti	964	20	87.0	806	2	T13551	penicillin binding
892	20	87.0	672	2	T00083	hypothetical prote	965	20	87.0	825	1	EDBEXD	hypothetical prote
893	20	87.0	674	2	T25876	hypothetical prote	966	20	87.0	826	2	E96720	immediate-early pr
894	20	87.0	675	2	F87022	ribonuclease E - S	967	20	87.0	829	2	S72366	probable alpha-amy
895	20	87.0	677	1	ADPG04	penicillin-binding	968	20	87.0	833	2	S48558	DNA topoisomerase
896	20	87.0	677	2	A60557	NADPH-ferrihemopro	969	20	87.0	834	2	B82940	probable membrane
897	20	87.0	678	1	RDRT04	NADPH-ferrihemopro	970	20	87.0	835	2	T47521	conserved hypotet
898	20	87.0	678	2	S27158	NADPH-ferrihemopro	971	20	87.0	835	2	A80238	respiratory burst
899	20	87.0	679	2	A25505	NADPH-ferrihemopro	972	20	87.0	836	1	S25218	protein T13H5.4 [i
900	20	87.0	683	2	JH0810	guanylate cyclase	973	20	87.0	841	2	G71814	outer membrane ush
901	20	87.0	684	2	T49436	hypothetical prote	974	20	87.0	842	2	S51513	hypothetical prote
902	20	87.0	687	2	S69733	PBSX prophage ORF	975	20	87.0	844	2	F84231	phosphoribosyl-AMP
903	20	87.0	688	2	S32961	hypothetical prote	976	20	87.0	844	2	G64704	hypothetical prote
904	20	87.0	691	2	E70906	probable beta-gluc	977	20	87.0	865	2	A83946	DNA mismatch repai
905	20	87.0	692	2	T21722	hypothetical prote	978	20	87.0	865	2	T09050	AC133 antigen - hu

979 20 87.0 865 2 AB0522  
 980 20 87.0 866 2 B85075  
 981 20 87.0 868 2 G54119  
 982 20 87.0 869 1 A28443  
 983 20 87.0 880 2 E69680  
 984 20 87.0 880 2 S51473  
 985 20 87.0 884 2 C70729  
 986 20 87.0 888 2 C90595  
 987 20 87.0 890 2 A48753  
 988 20 87.0 893 2 S63378  
 989 20 87.0 893 2 D81989  
 990 20 87.0 904 2 C83030  
 991 20 87.0 905 2 T40015  
 992 20 87.0 910 2 C86615  
 993 20 87.0 910 2 F72009  
 994 20 87.0 915 2 T26695  
 995 20 87.0 920 1 D48349  
 996 20 87.0 921 2 G02326  
 997 20 87.0 926 2 S36742  
 998 20 87.0 927 2 T47827  
 999 20 87.0 929 2 T32492  
 1000 20 87.0 950 2 T38777

## ALIGNMENTS

## RESULT 1

hypothetical protein NMA1220 [imported] - Neisseria meningitidis (strain Z2491 serogroup C)  
 C:Species: Neisseria meningitidis  
 C>Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
 C:Accession: C61890  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, J.; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, M.A.; Barrell, J.; Whitehead, S.; Barrell, J.; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, J.; Nature 404, 502-506, 2000  
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
 A:Reference number: A81775; MUID:2022556; PMID:10761919  
 A:Accession: C81890  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-87 <PAR>  
 A:Cross-references: GB:AL162755; GB:AL157959; NID:G7379742; PIDN:CAB84480.1; PID:G737990  
 A:Experimental source: serogroup A, strain Z2491  
 C:Genetics:  
 A:Gene: NMA1220

Query Match 100.0%; Score 23; DB 2; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 Db 46 DAHK 49

## RESULT 2

hypothetical protein MUCB1450.18 [imported] - Mycobacterium leprae  
 C:Species: Mycobacterium leprae  
 C>Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jan-2000  
 C:Accession: T44734  
 R:James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
 submitted to the EMBL Data Library, January 1998  
 A:Reference number: Z22831  
 A:Accession: T44734  
 A>Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-92 <JAM>  
 A:Cross-references: EMBL:AL035159; PIDN:CAA22702.1  
 A:Experimental source: cosmid B1450  
 C:Genetics:  
 A:Note: MUCB1450.18

Query Match 100.0%; Score 23; DB 2; Length 87;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 Db 46 DAHK 49

Query Match 100.0%; Score 23; DB 2; Length 92;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 Db 41 DAHK 44

## RESULT 3

hypothetical protein YPO3089 [imported] - Yersinia pestis (strain CO92)  
 C:Species: Yersinia pestis  
 C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
 C:Accession: AH0375  
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, J.; Nature 413, 523-527, 2001  
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A:Reference number: AB0001; MUID:21470413; PMID:11586360  
 A:Accession: AH0375  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-94 <KUR>  
 A:Cross-references: GB:AL590842; PIDN:CAC92331.1; PID:gl5981042; GSPDB:GN00175  
 C:Genetics:  
 A:Gene: YPO3089

Query Match 100.0%; Score 23; DB 2; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 Db 19 DAHK 22

## RESULT 4

transcription regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
 C:Species: Lactococcus lactis subsp. lactis  
 C>Date: 23-Mar-2001 #sequence\_revision 23-Mar-2001 #text\_change 03-Aug-2001  
 C:Accession: G86805  
 R:Boletín, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich, S.; Nature Res. 11, 731-753, 2001  
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis subsp. lactis strain IL1403.  
 A:Reference number: A86625; MUID:21235186; PMID:11337471  
 A:Accession: G86805  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-100 <STO>  
 A:Cross-references: GB:AF005176; PID:gl2724437; PIDN:AAK05545.1; GSPDB:GN00146  
 A:Experimental source: strain IL1403  
 C:Genetics:  
 A:Gene: yogl

Query Match 100.0%; Score 23; DB 2; Length 100;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 Db 18 DAHK 21

## RESULT 5

hypothetical protein - Deinococcus radiodurans (strain R1)  
 C:Species: Deinococcus radiodurans  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
 C:Accession: E75528

R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
 S.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Uterback, T.; Zaleski, C.; Ma  
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
 Science 286, 1571-1577, 1999  
 A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
 A;Reference number: A75250; MUID:20036896; PMID:10567266  
 A;Accession: E75528  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-102 <WHI>  
 A;Cross-references: GB:AE001896; GB:AE00513; NID:G6458032; PIDN:AAF09945.1; PID:G645804  
 A;Experimental source: strain R1  
 C;Genetics:  
 A;Gene: DR0355  
 A;Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 102;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 Db 49 DAHK 52

RESULT 6  
 G43258  
 phosphotransferase system enzyme II (EC 2.7.1.69), lactose-specific, factor III - Strept  
 N;Alternate names: phosphotransferase system enzyme III, lactose-specific  
 C;Species: Streptococcus mutans  
 C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 24-Nov-2003  
 C;Accession: G43258; S27705  
 R;Rosey, E.L.; Stewart, G.C.  
 J. Bacteriol. 174, 6159-6170, 1992  
 A;Title: Nucleotide and deduced amino acid sequences of the lacR, lacABCD, and lacPE gen  
 onents of the lactose operon of Streptococcus mutans.  
 A;Reference number: A43258; MUID:93015655; PMID:1400164  
 A;Accession: G43258  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-104 <ROS>  
 A;Cross-references: EMBL:M80797; NID:G153671; PIDN:AAA26908.1; PID:G153677  
 A;Note: sequence extracted from NCBI backbone (NCBIP:115206)  
 C;Genetics:  
 A;Gene: lacF  
 C;Superfamily: phosphotransferase system lactose/cellobiose-specific enzyme II,  
 C;Keywords: phosphoprotein; phosphotransferase

Query Match 100.0%; Score 23; DB 1; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 Db 52 DAHK 55

RESULT 7  
 T45101  
 H+-transporting two-sector ATPase (EC 3.6.3.14) chain H [imported] - Methanosarcina maze  
 C;Species: Methanosarcina mazei  
 C;Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 03-Jun-2002  
 R;Accession: T45101  
 R;Ruppert, C.; Wimmers, S.; Muller, V.  
 submitted to the EMBL Data Library, March 1998  
 A;Reference number: Z22913  
 A;Accession: T45101  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-109 <RUP>  
 A;Cross-references: EMBL:U47274; PIDN:AAC06380.1  
 A;Experimental source: strain Go1  
 C;Genetics:

A;Gene: ahaH  
 C;Keywords: hydrolase

Query Match 100.0%; Score 23; DB 2; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 Db 49 DAHK 52

RESULT 8  
 G97473  
 hypothetical protein AGR\_C\_1710 [imported] - Agrobacterium tumefaciens (strain C58, Cere  
 C;Species: Agrobacterium tumefaciens  
 C;Date: 30-Sep-2001 #sequence\_revision 30-Sep-2001 #text\_change 18-Nov-2002  
 C;Accession: G97473  
 R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorllo, B.; Goldman,  
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.;  
 Science 294, 2323-2328, 2001  
 A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum  
 A;Reference number: A97359; MUID:21608551; PMID:11743194  
 A;Accession: G97473  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-112 <KUR>  
 A;Cross-references: GB:AE007869; PIDN:AAK86744.1; PID:G15155938; GSPDB:GN00159  
 C;Genetics:  
 A;Gene: AGR\_C\_1710  
 A;Map position: circular chromosome

Query Match 100.0%; Score 23; DB 2; Length 112;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 Db 84 DAHK 87

RESULT 9  
 C82906  
 ribosome binding factor A UU321 [imported] - Ureaplasma urealyticum  
 C;Species: Ureaplasma urealyticum  
 C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
 C;Accession: C82906  
 R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.  
 submitted to GenBank, February 2000  
 A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mir  
 A;Reference number: A82870  
 A;Accession: C82906  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-116 <GLA>  
 A;Cross-references: GB:AE002129; GB:AF222894; NID:G6899292; PIDN:AAF30730.1; GSPDB:GN001  
 A;Experimental source: serovar 3; biovar 1  
 C;Genetics:  
 A;Gene: rbfA; UU321  
 A;Genetic code: GSG3

Query Match 100.0%; Score 23; DB 2; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 Db 53 DAHK 56

RESULT 10  
 B90155  
 hypothetical protein SS00150 [imported] - Sulfolobus solfataricus

C;Species: Sulfolobus solfataricus  
C;Date: 24-May-2001 #sequence\_revision 24-May-2001 #text\_change 24-May-2001  
C;Accession: B90155  
R;She, O.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Aways, M.J.; Chan-  
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.  
arrett, R.A.; Ragan, M.A.; Senses, C.W.; Van der Oost, J.  
submitted to GenBank, April 2001  
A;Description: Sulfolobus solfataricus complete genome.  
A;Reference number: A99139  
A;Accession: B90155  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-118 <KUR>  
A;Cross-references: GB:AE006641; NID:gl13813279; PIDN:AAK40497.1; GSPDB:GN00155  
C;Genetics:  
A;Gene: SS00150

Query Match 100.0%; Score 23; DB 2; Length 118;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DAHK 4  
Db 85 DAHK 88

RESULT 11  
T36836  
hypothetical protein SCI35.23 - Streptomyces coelicolor  
C;Species: Streptomyces coelicolor  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 04-Mar-2000  
C;Accession: T36836  
R;Oliver, K.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, September 1998  
A;Reference number: Z21615  
A;Accession: T36836  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-121 <OLI>  
A;Cross-references: EMBL:AL031541; PIDN:CAA20812.1; GSPDB:GN00070; SCOEDB:SCI35.23  
A;Experimental source: strain A3(2)  
C;Genetics:  
A;Gene: SCOEDB:SCI35.23  
C;Superfamily: Streptomyces coelicolor hypothetical protein SCI35.23

Query Match 100.0%; Score 23; DB 2; Length 121;  
Best Local Similarity 100.0%; Pred. No. 1.3e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DAHK 4  
Db 52 DAHK 55

RESULT 12  
C70965  
hypothetical protein Rv2647 - Mycobacterium tuberculosis (strain H37RV)  
C;Species: Mycobacterium tuberculosis  
C;Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C;Accession: C70965  
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.  
i Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.  
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A;Reference number: A70500; MUID:9829598; PMID:9634230  
A;Accession: C70965  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-122 <COL>  
A;Cross-references: GB:Z80225; GB:AL123456; NID:g3242265; PIDN:CAB02355.1; PID:e266520;  
A;Experimental source: strain H37RV

C;Genetics:  
A;Gene: Rv2647

Query Match 100.0%; Score 23; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DAHK 4  
Db 78 DAHK 81

RESULT 13  
C75371  
conserved hypothetical protein - Deinococcus radiodurans (strain R1)  
C;Species: Deinococcus radiodurans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 17-Mar-2000  
C;Accession: C75371  
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; M.  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A;Reference number: A75250; MUID:20036896; PMID:10567266  
A;Accession: C75371  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-122 <WHI>  
A;Cross-references: GB:AE002007; GB:AE000513; NID:g6459402; PIDN:AAF11196.1; PID:g64594  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DR1636  
A;Map position: 1

Query Match 100.0%; Score 23; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DAHK 4  
Db 68 DAHK 71

RESULT 14  
T06427  
aminopeptidase - tomato (fragment)  
C;Species: Lycopersicon esculentum (tomato)  
C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 08-Oct-1999  
C;Accession: T06427  
R;Aggelis, A.; Kanellis, A.K.  
submitted to the EMBL Data Library, March 1998  
A;Description: Isolation and expression studies of tomato aminopeptidase under low oxyg  
A;Reference number: Z15671  
A;Accession: T06427  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-124 <AGG>  
A;Cross-references: EMBL:AJ004922; NID:el284297; PIDN:CAA06222.1; PID:el284298  
A;Experimental source: cultivar Ailsa Craig  
C;Genetics:  
A;Gene: AMP

Query Match 100.0%; Score 23; DB 2; Length 124;  
Best Local Similarity 100.0%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 DAHK 4  
Db 94 DAHK 97

RESULT 15  
D81138

succinate dehydrogenase, cytochrome b556 chain NMB0948 [imported] - Neisseria meningitidis  
 C:Species: Neisseria meningitidis  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 02-Feb-2001  
 C:Accession: D81138; B81881  
 R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.  
 Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;  
 ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.  
 Science 287, 1809-1815, 2000  
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve  
 A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.  
 A:Reference number: A81000; MUID:2017555; PMID:10710307  
 A:Accession: D81138  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-125 <TET>  
 A:Cross-references: GB:AE002446; GB:AE002098; NID:g7226185; PIDN:AAF41354.1; PID:g722618  
 R:Experimental source: serogroup B, strain MCS8  
 R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
 ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
 Nature 404, 502-506, 2000  
 A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.  
 A:Reference number: A81775; MUID:20222556; PMID:10761919  
 A:Accession: B81881  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-125 <PAR>  
 A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84405.1; PID:g737983  
 R:Experimental source: serogroup A, strain Z2491  
 C:Genetics:  
 C:Gene: sdhC; NMB0948; NMA1143  
 C:Superfamily: succinate dehydrogenase 14K hydrophobic protein

Query Match 100.0%; Score 23; DB 2; Length 125;  
 Best Local Similarity 100.0%; Pred. NO. 1.4e+02;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 Db 92 DAHK 95

Search completed: September 9, 2004, 23:48:23  
 Job time : 62 secs



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OM protein - protein search, using sw model

Run on: September 9, 2004, 23:33:02 ; Search time 23 Seconds

(without alignments)  
9.056 Million cell updates/sec

Title: US-10-076-071-1

Perfect score: 23

Sequence: 1 DAHK 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	104	1	PTLA_STRUM
2	23	100.0	107	1	Y210_COREF
3	23	100.0	116	1	RBFA_UREPA
4	23	100.0	140	1	HBFA_RANES
5	23	100.0	149	1	FUR_VIBPA
6	23	100.0	149	1	FUR_VIBVU
7	23	100.0	151	1	HUTP_BACSU
8	23	100.0	156	1	ATPF_VIBVU
9	23	100.0	168	1	LCRH_YERPE
10	23	100.0	168	1	LCRH_YERPS
11	23	100.0	170	1	PHAF_CVACA
12	23	100.0	178	1	IPYR_BRAJA
13	23	100.0	196	1	SODF_TETPY
14	23	100.0	205	1	UBAI_CANAL
15	23	100.0	207	1	VG66_BPM15
16	23	100.0	207	1	YAFE_ECOLI
17	23	100.0	210	1	GTPI_BURBU
18	23	100.0	222	1	FSA_STREN
19	23	100.0	223	1	DEOC_MYCGE
20	23	100.0	224	1	DEOC_MYCPN
21	23	100.0	229	1	SOML_CYCLU
22	23	100.0	230	1	SOML_CARAU
23	23	100.0	230	1	SOML_HIPHI
24	23	100.0	230	1	SOML_ICTPU
25	23	100.0	230	1	SOML_SOLSE
26	23	100.0	231	1	SOML_SPAAU
27	23	100.0	231	1	SOM2_SPAUL
28	23	100.0	231	1	SOML_PAROL
29	23	100.0	231	1	SOML_SCIOC
30	23	100.0	231	1	SOML_SIGGU
31	23	100.0	232	1	SOML_ACITR
32	23	100.0	232	1	SOML_PROAN
33	23	100.0	233	1	SOML_ONCKE
					P26426 streptococ
					Q9full1 corynebacte
					Q9pqh0 ureaplasma
					P02134 rana escule
					O24755 vibrio para
					P33117 vibrio vuln
					P10943 bacillus su
					Q8ddh2 vibrio vuln
					P21207 yersinia pe
					P23995 yersinia ps
					O19896 cyanidium c
					Q89wy0 bradyrhizob
					P19666 tetrahymena
					P52495 candida alb
					Q05280 mycobacteri
					P30866 escherichia
					P81942 bufo bufo (
					Q77882 streptococ
					P47296 mycoplasma
					P09924 mycoplasma
					P45640 cyclopterus
					P79697 carassius a
					P45641 hippoglossu
					Q918j9 ictalurus p
					P45642 solea seneg
					P54863 sparus aura
					P79894 sparus aura
					P20362 paralichth
					Q9ygk7 sciaenops o
					Q9pwg4 siganus gut
					O33262 acipenser t
					O73847 protopterus
					P24405 oncorhynch

34	23	100.0	235	1	SOML_GADMO
35	23	100.0	236	1	Y608_PYRAB
36	23	100.0	236	1	YF52_PYRHO
37	23	100.0	237	1	Y450_MYCPN
38	23	100.0	238	1	DSBC_ERWCH
39	23	100.0	245	1	YGJ8_YEAST
40	23	100.0	246	1	NCAP_SFVS
41	23	100.0	261	1	TRMB_XANAC
42	23	100.0	263	1	1439_ARATH
43	23	100.0	266	1	10D2_FUNHE
44	23	100.0	271	1	YDHO_ECOLI
45	23	100.0	277	1	TNR4_HUMAN
46	23	100.0	283	1	PORI_CAEEL
47	23	100.0	283	1	Y43C_MYCPN
48	23	100.0	292	1	RBSB_HABIN
49	23	100.0	298	1	CC28_YEAST
50	23	100.0	298	1	ERA_RALSO
51	23	100.0	303	1	V212_FOWPV
52	23	100.0	305	1	E2BA_CAEEL
53	23	100.0	318	1	SYGA_MORCA
54	23	100.0	319	1	CNC7_HUMAN
55	23	100.0	319	1	CNC7_MOUSE
56	23	100.0	331	1	SYFA_XANAC
57	23	100.0	332	1	LDHB_ANGRO
58	23	100.0	332	1	LDHD_LACDE
59	23	100.0	343	1	NAGZ_YERPE
60	23	100.0	344	1	SFR6_HUMAN
61	23	100.0	345	1	D2D2_XENLA
62	23	100.0	345	1	KR1_SVVD
63	23	100.0	360	1	LPXB_HELPJ
64	23	100.0	360	1	LPXB_HELPY
65	23	100.0	361	1	PDAG_ARATH
66	23	100.0	366	1	YQCC_BACSU
67	23	100.0	370	1	LEU3_BRAJA
68	23	100.0	375	1	SR55_DROME
69	23	100.0	383	1	TGT_RALSO
70	23	100.0	389	1	BIOF_BACSU
71	23	100.0	389	1	VMSA_HBEVJ
72	23	100.0	390	1	TRA6_ENTFA
73	23	100.0	390	1	TRA6_STAAU
74	23	100.0	420	1	MTCL_HERAU
75	23	100.0	421	1	PHFL_DESVO
76	23	100.0	424	1	BCHN_RHOCA
77	23	100.0	425	1	VRK1_BRARE
78	23	100.0	428	1	HISX_BACTN
79	23	100.0	428	1	HISX_CAMJE
80	23	100.0	428	1	MTBA_BACAR
81	23	100.0	429	1	UTMP_SHEEP
82	23	100.0	431	1	HISX_VIBCH
83	23	100.0	431	1	HISX_VIBPA
84	23	100.0	431	1	HISX_VIBVU
85	23	100.0	437	1	ARLY_CLOAB
86	23	100.0	438	1	ARLY_CLOTE
87	23	100.0	438	1	HISX_SHEON
88	23	100.0	440	1	VRK1_XENLA
89	23	100.0	442	1	D2D1_XENLA
90	23	100.0	445	1	ADIC_ECO57
91	23	100.0	445	1	ADIC_ECOL6
92	23	100.0	445	1	ADIC_ECOLI
93	23	100.0	445	1	ADIC_SALTY
94	23	100.0	445	1	ADIC_SALTY
95	23	100.0	445	1	ADIC_SHIFL
96	23	100.0	449	1	SCRC_RAR
97	23	100.0	456	1	YMJ5_CAEEL
98	23	100.0	466	1	GID_BRUME
99	23	100.0	466	1	HISX_ARATH
100	23	100.0	469	1	HISX_BRAOC
101	23	100.0	470	1	IE63_HSVBB
102	23	100.0	470	1	IE63_HSVBK
103	23	100.0	472	1	GID_RHILO
104	23	100.0	472	1	GID_RHIME
105	23	100.0	473	1	GARI_HUMAN
106	23	100.0	474	1	GARI_MOUSE
					P21919 gadus morhu
					Q9v121 pyrococcus
					Q92220 pyrococcus
					P75127 mycoplasma
					P39691 erwinia chr
					P53146 saccharomyc
					P21793 sandfly fev
					Q8phf4 xanthomonas
					Q96299 arabidopsis
					P79747 fundulus he
					P76190 escherichia
					Q21752 caenorhabdi
					Q21752 caenorhabdi
					P51153 mycoplasma
					P44737 haemophilus
					P00546 saccharomyc
					Q9y010 ralstonia s
					Q8y523 fowlpox vir
					P34604 caenorhabdi
					P7892 moraxella c
					Q8tb37 homo sapien
					Q9cwe8 mus musculu
					Q8pje4 xanthomonas
					Q9ygl2 anguilla ro
					P26297 lactobacill
					Q8zf63 yersinia pe
					Q13247 homo sapien
					P34973 xenopus lae
					Q04543 simian vari
					Q25537 helicobacte
					Q22263 arabidopsis
					P45938 bacillus su
					Q89xi9 bradyrhizob
					P26686 drosophila
					Q8xvw4 ralstonia s
					P5556 bacillus su
					P17398 hepatitis b
					P59787 enterococc
					P1775 staphylococ
					P25263 herpetosiph
					P13629 desulfovibr
					P26164 rhodobacter
					Q72u81 brachydanio
					Q8ab9 bacteroides
					P19888 bacillus an
					P21814 ovis aries
					Q9f854 vibrio chol
					Q87q11 vibrio para
					Q8d8q0 vibrio vuln
					P97k65 clostridium
					P59616 clostridium
					Q8efb1 shewanella
					Q80x41 mus musculu
					P24628 xenopus lae
					P60063 escherichia
					P60062 escherichia
					P60061 escherichia
					P60065 salmonella
					P60066 salmonella
					P60064 shigella fl
					P23811 rattus norv
					P34481 caenorhabdi
					Q8ygt4 bruceella me
					Q9c5u8 arabidopsis
					P24236 brassica ol
					P28939 equine herp
					Q05906 equine herp
					Q98161 rhizobium l
					Q92q15 rhizobium m
					P24046 homo sapien
					P56475 mus musculu

107	23	100.0	474	1	GAR1_RAT	P50572	rattus norv	180	23	100.0	949	1	EMI3_HUMAN	Q98166	homo sapien	93816
108	23	100.0	477	1	SYC_RHIL0	O984x8	rhizobium 1	181	23	100.0	954	1	GSP_AGRIS	Q8ufd6	agrobacteri	93816
109	23	100.0	481	1	ARLY_METMP	O74026	methanococ	182	23	100.0	966	1	CAP1_MESCR	P10490	mesembryant	93816
110	23	100.0	481	1	GID_AGRIS	Q8uet6	agrobacteri	183	23	100.0	1002	1	REMC_MOUSE	P844x3	mus musculus	93816
111	23	100.0	485	1	ANGT_HUMAN	P01019	homo sapien	184	23	100.0	1025	1	LCAP_RAT	P7629	r leucyl-cy	93816
112	23	100.0	485	1	ANGT_PANTR	Q9qln8	pan troglod	185	23	100.0	1027	1	EB30_CABEL	P34441	caenorhabdi	93816
113	23	100.0	485	1	CALB_CAUCR	Q9a777	caulobacter	186	23	100.0	1046	1	RPOC_WEIHE	P96177	weissella h	93816
114	23	100.0	489	1	SPR4_MOUSE	Q8ve97	mus musculus	187	23	100.0	1054	1	RPOC_WEIPE	P96178	weissella h	93816
115	23	100.0	490	1	VGLY_LASSG	P17332	lassa virus	188	23	100.0	1129	1	UBPL_SCHPO	Q9utt1	schizosacch	93816
116	23	100.0	491	1	VGLY_LASSU	P08669	lassa virus	189	23	100.0	1134	1	YML7_YEAST	Q03735	saccharomyc	93816
117	23	100.0	494	1	PSD3_DROME	P25161	drosophila	190	23	100.0	1257	1	PER2_MOUSE	O54943	mus musculus	93816
118	23	100.0	494	1	SPR4_HUMAN	Q48170	homo sapien	191	23	100.0	1583	1	GCC2_HUMAN	Q81wj2	homo sapien	93816
119	23	100.0	497	1	RPN3_SCHPO	O42897	schizosacch	192	23	100.0	1607	1	MIPT_LYMET	Q25410	lynnaea sta	93816
120	23	100.0	498	1	GTA_NPVOP	O10302	orgyia pseu	193	23	100.0	1778	1	NI89_SCHPO	Q9utk4	schizosacch	93816
121	23	100.0	498	1	YDHF_SCHPO	Q92360	schizosacch	194	23	100.0	1803	1	YUL3_YEAST	P47024	saccharomyc	93816
122	23	100.0	503	1	VRK2_MOUSE	Q8bn21	mus musculus	195	23	100.0	1967	1	CHDA_HUMAN	Q9p2d1	homo sapien	93816
123	23	100.0	508	1	VRK2_HUMAN	Q86y07	homo sapien	196	23	100.0	2095	1	RPI_MOUSE	P56716	mus musculus	93816
124	23	100.0	510	1	MYIN_HAEIN	P44958	haemophilus	197	23	100.0	2156	1	RPI_HUMAN	P56715	homo sapien	93816
125	23	100.0	520	1	TUL2_HUMAN	O00295	homo sapien	198	23	100.0	2215	1	SORL_MOUSE	O88307	m sortilin-	93816
126	23	100.0	534	1	EHD1_HUMAN	Q9h4m9	homo sapien	199	23	100.0	2230	1	GOA4_HUMAN	Q13439	homo sapien	93816
127	23	100.0	534	1	EHD1_MOUSE	Q9vkv4	mus musculus	200	23	100.0	2670	1	IP3T_RAT	Q63269	rattus norv	93816
128	23	100.0	535	1	EHD3_MOUSE	Q9qxy6	mus musculus	201	23	100.0	2671	1	IP3T_HUMAN	Q14573	homo sapien	93816
129	23	100.0	535	1	CEI_AVEA	P40412	avena sativ	202	23	100.0	3079	1	IRA2_YEAST	P19158	saccharomyc	93816
130	23	100.0	541	1	EHD4_HUMAN	Q9h223	homo sapien	203	23	100.0	3084	1	MLL2_HUMAN	P19137	mus musculus	93816
131	23	100.0	541	1	EHD4_MOUSE	Q9egp2	mus musculus	204	23	100.0	5262	1	MACF_MOUSE	O14686	homo sapien	93816
132	23	100.0	543	1	EHD2_HUMAN	Q9hzn4	homo sapien	205	23	100.0	5327	1	MACF_MOUSE	Q9qzx0	mus musculus	93816
133	23	100.0	546	1	EHD3_HUMAN	Q9hzn3	homo sapien	206	23	100.0	5430	1	MACF_MOUSE	Q9upn3	homo sapien	93816
134	23	100.0	558	1	BCHD_RHOSH	O34845	rhodobacter	207	23	100.0	5938	1	MAC4_HUMAN	Q96pk2	homo sapien	93816
135	23	100.0	562	1	TRJM_PANAY	Q47861	pantosea 999	208	23	100.0	8797	1	SNE1_HUMAN	Q8af91	homo sapien	93816
136	23	100.0	595	1	YB85_SCHPO	O14301	schizosacch	209	23	100.0	88	1	S108_MOUSE	P27005	mus musculus	93816
137	23	100.0	605	1	CORO_CAEEL	Q21624	caenorhabdi	210	23	100.0	88	1	S108_MOUSE	P50115	rattus norv	93816
138	23	100.0	609	1	ALBU_HUMAN	P02768	homo sapien	211	23	100.0	104	1	PRIN_PSEAE	Q06552	pseudomonas	93816
139	23	100.0	620	1	YMO2_YEAST	Q03162	saccharomyc	212	23	100.0	106	1	YOB5_MYCLE	Q49723	mycobacteri	93816
140	23	100.0	625	1	THIC_XANCP	Q8p513	xanthomonas	213	23	100.0	119	1	CAD2_LISIN	P94887	listeria in	93816
141	23	100.0	625	1	THIC_XANCP	Q8p513	xanthomonas	214	23	100.0	119	1	MP2_NERDI	P80255	neris dive	93816
142	23	100.0	638	1	DNAK_BACTN	Q89yw6	bacteroides	215	23	100.0	120	1	HEMM_THERS	Q99y29	theromyzon	93816
143	23	100.0	638	1	DNAK_PRELO	Q939f1	prevotella	216	23	100.0	124	1	KABI_OLDAP	P56254	oldenlandia	93816
144	23	100.0	646	1	KPC1_APLCA	Q16974	aplysia cal	217	23	100.0	128	1	H2A3_CHICK	P35062	gallus gall	93816
145	23	100.0	679	1	HP1_METAC	Q8tj9a	methanosarc	218	23	100.0	128	1	H2A3_CHICK	P02263	gallus gall	93816
146	23	100.0	676	1	HP1_METMA	Q8p728	methanosarc	219	23	100.0	128	1	H2A_CAIMO	P13912	cairina mos	93816
147	23	100.0	685	1	HPA_NITEU	Q82tf3	nitrosomona	220	23	100.0	134	1	PRL_BUFA	P43001	bufo japoni	93816
148	23	100.0	695	1	PARB_CAUCR	O54479	caulobacter	221	23	100.0	137	1	NUSB_HAEDU	Q7vnd2	haemophilus	93816
149	23	100.0	702	1	LONH_HALNI	Q9hsc3	halobacteri	222	23	100.0	138	1	NUSB_BUCAL	Q8K9a2	buchnera ap	93816
150	23	100.0	702	1	YCBY_ECOLI	P75864	escherichia	223	23	100.0	138	1	NUSB_PHOOL	Q7n0j0	photobabu	93816
151	23	100.0	706	1	HPA_BRAJA	Q89k83	bradyrhizob	224	23	100.0	138	1	NUSB_YERPE	Q8zc42	yersinia pe	93816
152	23	100.0	711	1	CATE_PSEPU	P95539	pseudomonas	225	23	100.0	139	1	NUSB_ECOLI	P04381	escherichia	93816
153	23	100.0	711	1	HPA_THERIN	Q8rcx1	thermonaer	226	23	100.0	139	1	NUSB_SALTI	Q82x6	salmonella	93816
154	23	100.0	726	1	RNR_BUCAP	Q8K917	buchnera ap	227	23	100.0	139	1	NUSB_SALTY	Q8zrd3	salmonella	93816
155	23	100.0	731	1	BAF1_YEAST	P14164	saccharomyc	228	23	100.0	139	1	RS12_DROME	P80455	drosophila	93816
156	23	100.0	731	1	RNR_BUCAI	P57628	buchnera ap	229	23	100.0	143	1	NUSB_BUCAI	P57535	buchnera ap	93816
157	23	100.0	743	1	STB5_YEAST	P38699	saccharomyc	230	23	100.0	144	1	COPE_MOUSE	P59452	buchnera ap	93816
158	23	100.0	745	1	HGL2_ARATH	P46607	arabidopsis	231	23	100.0	144	1	NUSB_BUCMU	P57868	pasteurella	93816
159	23	100.0	753	1	CATE_ECOLI	P21179	escherichia	232	23	100.0	144	1	PHNO_ECOLI	P16691	escherichia	93816
160	23	100.0	759	1	GLQ2_ARATH	Q9sz11	arabidopsis	233	23	100.0	144	1	Y004_TREPA	Q22050	treponema p	93816
161	23	100.0	766	1	GLQ1_ARATH	Q9fj62	arabidopsis	234	23	100.0	145	1	Y060_CABEL	Q22634	caenorhabdi	93816
162	23	100.0	788	1	AD07_MOUSE	Q35227	mus musculus	235	23	100.0	145	1	NUSB_VIBFI	Q89g93	vibrio fisc	93816
163	23	100.0	789	1	AD07_RAT	Q63180	rattus norv	236	23	100.0	155	1	NUSB_VIBFI	Q87ru3	vibrio para	93816
164	23	100.0	791	1	Y046_UREPA	Q9p799	ureaplasma	237	23	100.0	155	1	NUSB_VIBVU	Q8dfa0	vibrio vuln	93816
165	23	100.0	799	1	SYFB_CAUCR	Q9a9e5	caulobacter	238	23	100.0	155	1	NUSB_VIBVU	Q7mm52	vibrio vuln	93816
166	23	100.0	813	1	RNR_ECOLI	P21499	escherichia	239	23	100.0	156	1	NUSB_VIBCH	Q9rxs6	deinococcus	93816
167	23	100.0	813	1	RNR_SHIFL	P30851	shigella fl	240	23	100.0	161	1	ISPF_DEIRA	P82186	mytilus edu	93816
168	23	100.0	814	1	KEX2_YEAST	P13134	saccharomyc	241	23	100.0	181	1	GUN_MYTED	Q82966	yersinia pe	93816
169	23	100.0	821	1	RNR_VIBCH	Q9kny1	vibrio chol	242	23	100.0	192	1	TRPG_YERPE	P29234	mustela vis	93816
170	23	100.0	825	1	SWI3_YEAST	P32591	saccharomyc	243	23	100.0	193	1	PRL_MUSVI	Q98166	pseudomonas	93816
171	23	100.0	831	1	RPRR_CHICK	Q04594	gallus gall	244	23	100.0	196	1	AMIE_PSEAE	Q9h412	halobacteri	93816
172	23	100.0	835	1	RNR_VIBPA	P40611	vibrio para	245	23	100.0	196	1	R1SE_HALNI	Q93090	chelonina my	93816
173	23	100.0	865	1	AC02_ECOLI	P36683	escherichia	246	23	100.0	198	1	PRL_CHEMY	P55751	crocodilus m	93816
174	23	100.0	871	1	IF2_CAMJE	Q9piz1	campylobact	247	23	100.0	199	1	PRL1_ALLMI	P55753	alligator m	93816
175	23	100.0	876	1	TOP1_VIBCH	Q9kxb2	vibrio chol	248	23	100.0	199	1	PRL1_CRONO	P55752	alligator m	93816
176	23	100.0	883	1	RPOL_BPT7	P00573	bacterioph	249	23	100.0	199	1	PRL2_ALLMI	P55754	crocodilus	93816
177	23	100.0	884	1	RPOL_BPT3	P07659	bacterioph	250	23	100.0	199	1	PRL2_CRONO	P55754	crocodilus	93816
178	23	100.0	898	1	UBPE_DROME	Q24574	drosophila	251	23	100.0	199	1	PRL2_CRONO	P55754	crocodilus	93816
179	23	100.0	906	1	RPOL_BPK11	P18147	bacterioph	252	23	100.0	199	1	PRL2_CRONO	P55754	crocodilus	93816



253	1	PRL_CAMDR	199	87.0	20	P22393 camelus dro	326	20	87.0	270	1	DLHH_SALTY	Q916m9 salmonella
254	1	PRL_HORSE	199	87.0	20	P12420 equus cabal	327	20	87.0	270	1	SFR5_MOUSE	Q5326 mus musculus
255	1	PRL_LOXAF	199	87.0	20	P10765 loxodonta a	328	20	87.0	271	1	ATFI_HUMAN	P18846 homo sapien
256	1	PS22_ARATH	199	87.0	20	O24633 arabidopsis	329	20	87.0	272	1	SFR5_HUMAN	Q13243 homo sapien
257	1	PRL2_OREMO	200	87.0	20	P09318 oreochromis	330	20	87.0	280	1	EPHB_RHOGO	Q47230 r cis-2,3-d
258	1	PS21_ARATH	204	87.0	20	O23714 arabidopsis	331	20	87.0	287	1	EUTC_PRESM	Q889m3 pseudomonas
259	1	PSB2_TRYBB	206	87.0	20	Q9nbc6 trypanosoma	332	20	87.0	292	1	Y125_MYCTU	Q50608 mycobacteri
260	1	PRL_HYPNO	207	87.0	20	P35395 hypophthalm	333	20	87.0	296	1	ERA_CLOAB	Q97j15 clostridium
261	1	YL95_RALSO	207	87.0	20	P58634 ralstonia s	334	20	87.0	298	1	PANB_BRAJA	Q9ame0 bradyrhizob
262	1	PRL_ANGAN	209	87.0	20	P33096 anguilla an	335	20	87.0	300	1	HAP2_KLUTA	P53768 kluyveromyc
263	1	FLPA_HALN1	210	87.0	20	Q9nqg3 halobacteri	336	20	87.0	300	1	KRB1_VACCC	P25055 vaccinia vi
264	1	PRL2_ONCKE	210	87.0	20	P09584 oncorhynch	337	20	87.0	300	1	KRB1_VACCV	P16913 vaccinia vi
265	1	PRL2_ONCKT	210	87.0	20	Q91364 oncorhynch	338	20	87.0	300	1	KRB1_VARV	P33800 variola vir
266	1	PRL_CARAU	210	87.0	20	P87495 garassius a	339	20	87.0	302	1	YIAL_PSESS	P18205 pseudomonas
267	1	PRL_CORAU	210	87.0	20	P34181 coregonus a	340	20	87.0	303	1	YN37_ARCFU	O27947 archaeoglob
268	1	PRL_CYPCA	210	87.0	20	P09585 cyprinus ca	341	20	87.0	304	1	YR06_CABEL	Q92943 caenorhabdi
269	1	PRL_HYPNO	210	87.0	20	P29235 hypophthalm	342	20	87.0	307	1	COPE_BOVIN	Q28104 bos taurus
270	1	PRL_ONCMY	210	87.0	20	P21993 oncorhynch	343	20	87.0	307	1	COPE_CRIGR	Q60445 cricetus
271	1	PRL_SALSA	210	87.0	20	P48096 salmo salar	344	20	87.0	307	1	COPE_HUMAN	O14579 homo sapien
272	1	PRL1_ONCKE	211	87.0	20	P09583 oncorhynch	345	20	87.0	308	1	ILVE_ECOLI	P00510 escherichia
273	1	PRL_PAROL	211	87.0	20	Q9ygv6 paralichthy	346	20	87.0	308	1	ILVE_SALTY	P15168 salmonella
274	1	PRL1_OREMO	212	87.0	20	P09319 oreochromis	347	20	87.0	309	1	CYP9_CABEL	Q09637 caenorhabdi
275	1	PRL_DICLA	212	87.0	20	P48249 dicentrarch	348	20	87.0	311	1	CYSM_BACSU	Q34476 bacillus su
276	1	PRL_ICTFU	212	87.0	20	P51904 ictalurus p	349	20	87.0	313	1	PIP_XANCI	P52279 xanthomonas
277	1	PRL_SPARU	212	87.0	20	Q93337 sparus aura	350	20	87.0	315	1	FLIM_BUCAI	P57182 buchnera ap
278	1	PSB2_ORYSA	212	87.0	20	Q91st6 oryza sativ	351	20	87.0	317	1	CC28_CANAL	P43063 candida alb
279	1	RPSD_MYCTU	212	87.0	20	Q50712 mycobacteri	352	20	87.0	317	1	YMT8_YEAST	Q04659 saccharomyc
280	1	GPH_RHOSH	218	87.0	20	P35650 rhodobacter	353	20	87.0	319	1	FLSX_CHLMO	Q9p1b1 chlamydia m
281	1	MAD_HUMAN	221	87.0	20	Q05195 homo sapien	354	20	87.0	321	1	PLSX_CHLTR	O48177 chlamydia t
282	1	FFP_BACSU	224	87.0	20	Q9f4f7 bacillus su	355	20	87.0	323	1	RLAO_LELIN	P39097 leishmania
283	1	LP14_BACSU	224	87.0	20	P39144 bacillus su	356	20	87.0	331	1	YB94_METHH	O27262 methanobact
284	1	SFP_BACSU	224	87.0	20	P39135 bacillus su	357	20	87.0	332	1	CREM_HUMAN	Q03060 homo sapien
285	1	PRL_MESAU	226	87.0	20	P37884 mesocricetu	358	20	87.0	336	1	DUSA_PSEPK	Q88kx0 pseudomonas
286	1	PRL_MOUSE	226	87.0	20	P06879 mus musculu	359	20	87.0	336	1	LEGC_HUMAN	Q96d0 homo sapien
287	1	PRL_RAT	226	87.0	20	P01237 rattus norv	360	20	87.0	338	1	GPDA_STRPN	Q97nf1 streptococc
288	1	GPH_RHILO	227	87.0	20	Q98m18 rhizobium l	361	20	87.0	338	1	GPDA_STRPN	Q8dn59 streptococc
289	1	PRL_HUMAN	227	87.0	20	P01236 homo sapien	362	20	87.0	341	1	CREM_MOUSE	P27699 mus musculu
290	1	PRL_MACMU	227	87.0	20	P55151 macaca mula	363	20	87.0	341	1	CREM_RAT	Q03061 rattus norv
291	1	PRL_RABIT	227	87.0	20	Q28632 coryctolagus	364	20	87.0	341	1	NAGZ_ECO57	P58067 escherichia
292	1	PRL_MONDO	228	87.0	20	O62819 monodelphis	365	20	87.0	341	1	NAGZ_ECOL6	Q8fin2 escherichia
293	1	PRL_TRIVU	228	87.0	20	O62781 trichosurus	366	20	87.0	341	1	NAGZ_ECOLI	P75949 escherichia
294	1	SOML_ANGAN	228	87.0	20	Q90216 anguilla an	367	20	87.0	341	1	NAGZ_SALTI	Q8z716 salmonella
295	1	PRL_CHICK	229	87.0	20	P14676 gallus gall	368	20	87.0	341	1	NAGZ_SALTY	O8zq06 salmonella
296	1	PRL_FELCA	229	87.0	20	P46403 felis silve	369	20	87.0	344	1	CREM_CANFA	P79145 canis fami
297	1	PRL_MELGA	229	87.0	20	P17572 meleagris g	370	20	87.0	344	1	VPO_EPP2	P25480 bacterioph
298	1	PRL_EIG	229	87.0	20	P01238 sus scrofa	371	20	87.0	344	1	Y496_MYCTU	Q11161 mycobacteri
299	1	YC22_ARATH	232	87.0	20	O81916 arabidopsis	372	20	87.0	345	1	DHAS_MYCTU	P37049 mycobacteri
300	1	PYRH_MYCPN	235	87.0	20	P75165 mycoplasma	373	20	87.0	348	1	TRPD_CORGL	P06559 corynebacte
301	1	Y141_METHH	236	87.0	20	O26244 methanobact	374	20	87.0	349	1	ESR1_ANOCA	Q9yht3 anolis caro
302	1	OPAJ_NEIGO	237	87.0	20	Q04882 neisseria g	375	20	87.0	351	1	CBF1_YEAST	P17106 saccharomyc
303	1	OPAK_NEIGO	237	87.0	20	Q04880 neisseria g	376	20	87.0	351	1	HSF3_LYCPE	P41132 lycopersico
304	1	YG02_METKA	237	87.0	20	Q8tu29 methanopyru	377	20	87.0	356	1	IRXH_CABEL	Q93348 caenorhabdi
305	1	HS6A_DRONE	238	87.0	20	P05812 drosophila	378	20	87.0	357	1	HRCU_RALSO	P37652 ralstonia s
306	1	RESB_BACSU	240	87.0	20	P35163 bacillus su	379	20	87.0	358	1	V044_FOWPV	Q9j5f9 fowlpox vir
307	1	FKBY_HABIN	241	87.0	20	P44760 haemophilus	380	20	87.0	358	1	Y502_MYCTE	Q11167 mycobacteri
308	1	YK88_SCHPO	241	87.0	20	O14304 schizosacch	381	20	87.0	361	1	AROB_MYCLE	Q9ccs4 mycobacteri
309	1	YH77_ARCFU	245	87.0	20	O28497 archaeoglob	382	20	87.0	361	1	IE63_PVKA	Q85232 pseudorabie
310	1	YSE0_STRCO	250	87.0	20	Q9zbn3 streptomyce	383	20	87.0	362	1	AROB_MYCTU	P36919 mycobacteri
311	1	Y264_STRAU	251	87.0	20	Q9x4h5 streptomyce	384	20	87.0	363	1	ATZD_PSESD	P58329 pseudomonas
312	1	YDA6_SCHPO	252	87.0	20	Q10348 schizosacch	385	20	87.0	363	1	CYA2_RHIME	Q52915 rhizobium m
313	1	MODA_HABIN	254	87.0	20	P45323 haemophilus	386	20	87.0	364	1	P16P_XANFL	P23014 xanthobacte
314	1	NCAP_UUK	254	87.0	20	P22025 uukuniemi v	387	20	87.0	365	1	SRP2_SCHPO	P78814 schizosacch
315	1	GLO2_RHOB	255	87.0	20	P05446 rhodopsedu	388	20	87.0	367	1	Y502_MYCLB	P54878 mycobacteri
316	1	MTNA_MYCTU	255	87.0	20	Q10889 mycobacteri	389	20	87.0	375	1	PER_DROCP	P91607 drosophila
317	1	GLO2_RHOCA	256	87.0	20	P96981 rhodobacter	390	20	87.0	380	1	YH07_PASMU	Q9ckb7 pasteurella
318	1	MODA_ECOLI	257	87.0	20	P37329 escherichia	391	20	87.0	382	1	ACBC_ACTS5	Q9zae9 actinoplan
319	1	NADC_ARCFU	258	87.0	20	O28439 archaeoglob	392	20	87.0	382	1	ISDF_CAUCR	Q9a715 c ispd/ispf
320	1	DPHB_METHH	264	87.0	20	O27902 methanobact	393	20	87.0	386	1	INTB_ECOLI	P39347 escherichia
321	1	SUEL_PYRAE	266	87.0	20	Q8zu79 pyrobaculum	394	20	87.0	398	1	KBL_ECOLI	P07912 escherichia
322	1	STO3_CABEL	267	87.0	20	Q20657 caenorhabdi	395	20	87.0	398	1	KBL_SALTY	P37419 salmonella
323	1	ATFI_MOUSE	269	87.0	20	P81269 mus musculu	396	20	87.0	400	1	ASSY_SYNY3	P77973 synechocyst
324	1	SFR5_RAT	269	87.0	20	Q09167 rattus norv	397	20	87.0	400	1	ISDF_AGR5	O8uff4 a ispd/ispf
325	1	DLHH_SALTI	270	87.0	20	Q8z3b8 salmonella	398	20	87.0	401	1	ASSY_SYNEL	Q8dky7 synechococc

399	20	87.0	402	1	CPXF_STRGO	P18327 streptomyce	472	20	87.0	538	1	IF3C_EUGGR	P36177 euglena gra
400	20	87.0	402	1	VP2_HPV65	O07851 human papil	473	20	87.0	547	1	YJDB_ECOLI	P30845 escherichia
401	20	87.0	403	1	MTB1_BREP	P10283 brevibacter	474	20	87.0	547	1	YJDB_SALTY	P36555 salmonella
402	20	87.0	404	1	RSPA_ECOLI	P14926 escherichia	475	20	87.0	557	1	ILVD_NITEU	O82xv7 nitrosomona
403	20	87.0	406	1	FABB_ECOLI	O89a57 buchnera ap	476	20	87.0	560	1	ILVD_SYNEU	O8k4l3 synecococc
404	20	87.0	408	1	DROB_BUCBP	P79385 sus scrofa	477	20	87.0	573	1	301D_COMTE	Q08401 comamonas t
405	20	87.0	409	1	MFGM_PIG	O92552 homo sapien	478	20	87.0	575	1	NRD1_ERWCH	P33693 erwinia chr
406	20	87.0	411	1	R227_HUMAN	Q92552 homo sapien	479	20	87.0	575	1	RECJ_ERWCH	P33693 erwinia chr
407	20	87.0	415	1	PIC1_HUMAN	Q92552 homo sapien	480	20	87.0	577	1	MTG8_MOUSE	O61909 mus musculu
408	20	87.0	416	1	PIC1_MOUSE	Q62083 mus musculu	481	20	87.0	578	1	MM17_MOUSE	Q92552 mus musculu
409	20	87.0	416	1	PIC1_RAT	Q92552 mus musculu	482	20	87.0	579	1	ESR1_SPAAU	Q92552 mus musculu
410	20	87.0	416	1	THAA_PAROL	Q91241 paralichthy	483	20	87.0	581	1	ESR1_PAGMA	P07362 pagrus mayo
411	20	87.0	416	1	THAA_HIPHI	Q91241 paralichthy	484	20	87.0	581	1	PRIM_SALTY	O41332 salmonella
412	20	87.0	422	1	KXSI_STRCN	O02578 streptomyce	485	20	87.0	583	1	ESR1_ORENI	P50240 oreochromis
413	20	87.0	424	1	MS11_ARATH	O22467 arabidopsis	486	20	87.0	585	1	ESR1_ORENI	Q9yh33 oreochromis
414	20	87.0	431	1	NRKA_TRYBB	O08942 trypanosoma	487	20	87.0	586	1	ESR1_XENLA	P81559 xenopus lae
415	20	87.0	431	1	NRKB_TRYBB	O03428 trypanosoma	488	20	87.0	587	1	ESR1_POEUG	P91250 poephila gu
416	20	87.0	438	1	NRK1_HORVU	P00693 hordeum vul	489	20	87.0	589	1	ESR1_CHICK	Q91250 poephila gu
417	20	87.0	440	1	SCRC_HUMAN	P47872 homo sapien	490	20	87.0	590	1	YMW7_YEAST	P32612 gallus gall
418	20	87.0	442	1	MNTH_RALSO	O8xsf6 ralstonia s	491	20	87.0	592	1	YMW7_YEAST	P32612 gallus gall
419	20	87.0	443	1	AM2A_ORYSA	P27935 oryza sativ	492	20	87.0	594	1	ESR1_HORSE	P34294 caenorhabdi
420	20	87.0	445	1	AMC2_ORYSA	P27941 oryza sativ	493	20	87.0	595	1	ESR1_HUMAN	Q9tv98 equus cabal
421	20	87.0	448	1	SCRC_RABIT	O46502 oryctolagus	494	20	87.0	595	1	ESR1_MESAU	P03372 homo sapien
422	20	87.0	448	1	GCSA_BACSU	P54376 bacillus su	495	20	87.0	595	1	ESR1_PIG	Q92zj5 mesocricetu
423	20	87.0	448	1	YG4Q_YEAST	P50079 saccharomyc	496	20	87.0	599	1	ESR1_MOUSE	Q23040 sus scrofa
424	20	87.0	451	1	PRPE_BACSU	P32959 bacillus su	497	20	87.0	600	1	ESR1_RAT	P19785 mus musculu
425	20	87.0	463	1	ALRY_CHLTE	O8xdj5 chlorobium	498	20	87.0	601	1	NCPR_SALTR	P06211 rattus norv
426	20	87.0	466	1	UXAC_BRUME	O8ydc2 brucella me	499	20	87.0	604	1	MTG8_HUMAN	P19618 salmo trutt
427	20	87.0	466	1	UXAC_BRUSU	O8fvm4 brucella su	500	20	87.0	606	1	WDRI_HUMAN	O06455 homo sapien
428	20	87.0	469	1	UXAC_RHILO	Q98ew1 rhizobium l	501	20	87.0	606	1	WDRI_MOUSE	O89342 mus musculu
429	20	87.0	469	1	UXAC_RHIME	Q92v04 rhizobium m	502	20	87.0	608	1	WDRI_CHICK	O93277 gallus gall
430	20	87.0	471	1	MURD_STRCO	O92z99 streptomyce	503	20	87.0	609	1	WDRI_MOUSE	O93277 gallus gall
431	20	87.0	479	1	CATA_DESYM	O92z99 streptomyce	504	20	87.0	609	1	WDRI_MOUSE	O93277 gallus gall
432	20	87.0	479	1	CATA_PSEPU	O59714 pseudomonas	505	20	87.0	614	1	MGM_EUBA	O59268 eubacterium
433	20	87.0	480	1	RADA_MYCTU	O53570 mycobacteri	506	20	87.0	617	1	ESR1_ICTPU	Q9yhz7 ictalurus p
434	20	87.0	482	1	CATA_BACSU	P26901 bacillus su	507	20	87.0	620	1	ESR1_ORYLA	P21910 xenopus lae
435	20	87.0	482	1	CATA_ONCVE	Q27710 onchocerca	508	20	87.0	623	1	LM2_XENLA	P21910 xenopus lae
436	20	87.0	482	1	CATA_PSEAE	O52762 pseudomonas	509	20	87.0	631	1	SVR_HAI1	Q9hnh2 halobacteri
437	20	87.0	483	1	BCA_STRVL	P33569 streptomyce	510	20	87.0	640	1	PTMA_BUCBP	O89a36 buchnera ap
438	20	87.0	484	1	CATA_PROMI	P42321 proteus mir	511	20	87.0	649	1	PTMA_BUCBP	O8k911 buchnera ap
439	20	87.0	485	1	YB47_MYCPN	P75139 mycoplasma	512	20	87.0	650	1	CC45_YEAST	Q08032 saccharomyc
440	20	87.0	487	1	CATA_STRCO	Q92598 streptomyce	513	20	87.0	663	1	PD11_HUMAN	Q9ulc6 homo sapien
441	20	87.0	489	1	VGLY_MOPEI	P19240 moepla viru	514	20	87.0	664	1	UL47_HSV1P	P08313 herpes simp
442	20	87.0	492	1	CPAC_MOUSE	P56593 mus musculu	515	20	87.0	674	1	RNE_SYNYF	P72656 synecocyst
443	20	87.0	492	1	MURE_STAAC	O86491 staphylococ	516	20	87.0	676	1	NCPR_HUMAN	P16435 homo sapien
444	20	87.0	494	1	CATA_RHIME	P95631 rhizobium m	517	20	87.0	677	1	NCPR_CAVPO	P16435 homo sapien
445	20	87.0	494	1	CPA6_HUMAN	P11509 homo sapien	518	20	87.0	677	1	NCPR_MOUSE	P37040 mus musculu
446	20	87.0	494	1	MURE_STAAM	Q99v74 staphylococ	519	20	87.0	677	1	NCPR_PIG	P04175 sus scrofa
447	20	87.0	494	1	MURE_STAAM	Q99v74 staphylococ	520	20	87.0	677	1	NCPR_PIG	P00388 rattus norv
448	20	87.0	494	1	MURE_STAAP	Q8nxc2 staphylococ	521	20	87.0	679	1	NCPR_RABIT	P00389 oryctolagus
449	20	87.0	498	1	CATA_BRUME	Q59170 brucella me	522	20	87.0	683	1	CYGH_DROME	Q07093 drosophila
450	20	87.0	498	1	CATA_BRUSU	Q8fw40 brucella su	523	20	87.0	687	1	XKDV_BACSU	P54341 bacillus su
451	20	87.0	501	1	CP36_RABIT	P11707 oryctolagus	524	20	87.0	688	1	YB9F_YEAST	P38338 saccharomyc
452	20	87.0	501	1	CP3V_MESAU	O70537 mesocricetu	525	20	87.0	692	1	GYRB_BABBA	P94281 bartonella
453	20	87.0	503	1	CP33_HUMAN	P05184 homo sapien	526	20	87.0	693	1	UL47_HSV1P	P10231 herpes simp
454	20	87.0	503	1	CP39_RAT	P15338 rattus norv	527	20	87.0	697	1	SM2A_SCHGR	Q9xzc8 schistocerc
455	20	87.0	503	1	NUSA_RICPR	Q92z27 rickettsia	528	20	87.0	706	1	SM2A_DROME	Q24323 drosophila
456	20	87.0	504	1	CP341_MOUSE	Q9jma7 mus musculu	529	20	87.0	706	1	UL17_HSV1P	P28950 equine heip
457	20	87.0	504	1	CP3G_MOUSE	Q64481 mus musculu	530	20	87.0	719	1	VM3_REOVD	P12419 reovirus (t
458	20	87.0	509	1	P233_HUMAN	Q9n220 homo sapien	531	20	87.0	723	1	TR2M_AGRVI	Q04564 agrobacteri
459	20	87.0	512	1	UGTB_CAEEL	Q22180 caenorhabdi	532	20	87.0	733	1	PSAB_ODOSI	P49480 odontella s
460	20	87.0	514	1	CP23_DROME	Q01520 drosophila	533	20	87.0	734	1	PSAB_GUTH	O78507 guillardia
461	20	87.0	514	1	CP24_RAT	Q91228 rattus norv	534	20	87.0	734	1	PSAB_PORPU	P51285 porphyra pu
462	20	87.0	514	1	IMD1_MOUSE	P50096 mus musculu	535	20	87.0	735	1	REIA_BACSU	O54408 bacillus su
463	20	87.0	515	1	CATA_YEAST	P15202 saccharomyc	536	20	87.0	740	1	AD02_YACFA	Q28478 macaca fasc
464	20	87.0	523	1	PUR9_MYCTU	P71553 m bifunctio	537	20	87.0	740	1	NLDL_HUMAN	Q9uq11 homo sapien
465	20	87.0	525	1	ESR1_MICUN	P57753 micropogoni	538	20	87.0	749	1	TR2M_AGRRH	Q09109 agrobacteri
466	20	87.0	526	1	SRC_RSVH1	P25020 rous sarcom	539	20	87.0	752	1	PSAA_CVACA	Q9t1q5 cyanidium c
467	20	87.0	526	1	SRC_RSV1	P00526 rous sarcom	540	20	87.0	754	1	MES3_CAEEL	Q10665 caenorhabdi
468	20	87.0	527	1	PUR9_MYCLE	Q925h5 m bifunctio	541	20	87.0	755	1	TR2M_AGR4T	P04029 agrobacteri
469	20	87.0	527	1	PUR9_MYCPA	Q9rajs m bifunctio	542	20	87.0	755	1	TR2N_AGRVI	P25017 agrobacteri
470	20	87.0	527	1	RHGB_ASPAC	Q00019 aspergillus	543	20	87.0	761	1	APG3_YEAST	P39925 saccharomyc
471	20	87.0	534	1	EK11_YEAST	Q03764 saccharomyc	544	20	87.0	763	1	PEPX_LACLA	Q9c601 lactococcus

545	1	765	87.0	20	618	P11387	homo sapien
546	1	767	87.0	20	619	Q01037	herpesvirus
547	1	767	87.0	20	620	Q07226	herpes simp
548	1	767	87.0	20	621	Q07050	cricetulus
549	1	767	87.0	20	622	Q04750	mus musculus
550	1	768	87.0	20	623	Q08797	rattus norv
551	1	770	87.0	20	624	P09284	varicella-z
552	1	772	87.0	20	625	P52183	schistocerc
553	1	776	87.0	20	626	Q11177	caenorhabdi
554	1	780	87.0	20	627	P06490	herpes simp
555	1	785	87.0	20	628	P10212	herpes simp
556	1	785	87.0	20	629	P12835	herpes simp
557	1	789	87.0	20	630	O18f70	bruceella su
558	1	792	87.0	20	631	Q8ybl8	bruceella me
559	1	792	87.0	20	632	Q67837	aquifex ae
560	1	795	87.0	20	633	Q13471	kluyveromyc
561	1	803	87.0	20	634	P09959	saccharomyc
562	1	809	87.0	20	635	Q8pce0	xanthomonas
563	1	825	87.0	20	636	P28284	herpes simp
564	1	829	87.0	20	637	P41512	xenopus lae
565	1	842	87.0	20	638	P45353	picchia past
566	1	852	87.0	20	639	Q9np71	homo sapien
567	1	865	87.0	20	640	Q9kac0	bacillus ha
568	1	865	87.0	20	641	Q43490	homo sapien
569	1	868	87.0	20	642	P43012	haemophilus
570	1	869	87.0	20	643	P05374	saccharomyc
571	1	880	87.0	20	644	Q3496	bacillus su
572	1	880	87.0	20	645	Q06708	saccharomyc
573	1	884	87.0	20	646	Q50654	mycobacteri
574	1	884	87.0	20	647	P59974	mycobacteri
575	1	893	87.0	20	648	P53739	saccharomyc
576	1	905	87.0	20	649	Q74787	schizosacch
577	1	911	87.0	20	650	P96315	bacillus th
578	1	916	87.0	20	651	Q8csx1	staphylococ
579	1	920	87.0	20	652	Q04454	herpesvirus
580	1	925	87.0	20	653	Q13469	homo sapien
581	1	926	87.0	20	654	P37278	synechococ
582	1	954	87.0	20	655	Q13474	homo sapien
583	1	959	87.0	20	656	P54881	mycobacteri
584	1	968	87.0	20	657	Q11171	mycobacteri
585	1	970	87.0	20	658	Q04222	comamonas t
586	1	988	87.0	20	659	P06694	escherichia
587	1	1008	87.0	20	660	P36048	saccharomyc
588	1	1019	87.0	20	661	P22472	rice dwarf
589	1	1020	87.0	20	662	Q98630	rice dwarf
590	1	1029	87.0	20	663	Q9b25	homo sapien
591	1	1032	87.0	20	664	Q14709	homo sapien
592	1	1032	87.0	20	665	Q9eq3	mus musculus
593	1	1049	87.0	20	666	Q07468	saccharomyc
594	1	1052	87.0	20	667	Q05397	homo sapien
595	1	1055	87.0	20	668	P29322	homo sapien
596	1	1055	87.0	20	669	Q35346	rattus norv
597	1	1060	87.0	20	670	P28025	xenopus lae
598	1	1061	87.0	20	671	P06538	human adeno
599	1	1064	87.0	20	672	Q9nx02	homo sapien
600	1	1064	87.0	20	673	Q60591	mus musculus
601	1	1067	87.0	20	674	Q91783	xenopus lae
602	1	1068	87.0	20	675	Q91738	xenopus lae
603	1	1070	87.0	20	676	Q15063	homo sapien
604	1	1075	87.0	20	677	P16023	zea mays (m
605	1	1076	87.0	20	678	Q9xps7	tritium ae
606	1	1090	87.0	20	679	P34152	mus musculus
607	1	1107	87.0	20	680	P36324	rasberry r
608	1	1122	87.0	20	681	P05684	human adeno
609	1	1155	87.0	20	682	P06578	bacillus th
610	1	1159	87.0	20	683	Q09904	schizosacch
611	1	1174	87.0	20	684	P52647	escherichia
612	1	1178	87.0	20	685	P05068	bacillus th
613	1	1188	87.0	20	686	P48311	human adeno
614	1	1193	87.0	20	687	P87503	human adeno
615	1	1194	87.0	20	688	P09252	varicella-z
616	1	1200	87.0	20	689	Q09530	caenorhabdi
617	1	1235	87.0	20	690	P04293	herpes simp
P07917	herpes simp						
P04292	herpes simp						
P09854	herpes simp						
P07918	herpes simp						
P11369	mus musculus						
Q26255	c trifuncti						
Q9wu60	mus musculus						
O75882	homo sapien						
Q99m80	mus musculus						
Q97822	streptococc						
Q8dras	streptococc						
Q14522	homo sapien						
Q8k558	streptococc						
Q8nb25	streptococc						
Q8ndf9	streptococc						
Q8cx24	streptococc						
Q10978	mycobacteri						
Q02004	dugbe virus						
P90761	caenorhabdi						
O14647	homo sapien						
O14674	homo sapien						
Q61292	mus musculus						
P09848	homo sapien						
P42694	homo sapien						
Q03149	emeritocella						
P23467	homo sapien						
Q93971	caenorhabdi						
P37800	toscana vir						
P15508	mus musculus						
P11277	homo sapien						
Q9eq60	rattus norv						
O88427	mus musculus						
Q00763	homo sapien						
P33892	saccharomyc						
P25391	homo sapien						
Q05470	bacillus su						
Q9pu36	gallus gall						
P81999	canis famil						
O14061	homo sapien						
P56394	mus musculus						
P81045	sus scrofa						
P24661	vicia faba						
P22151	neurospora						
P01065	vicia angus						
P03715	bacterioph						
P10836	protophormi						
P45658	androctonus						
Q97131	clostridium						
P18684	protophormi						
Q05256	mycobacteri						
P32156	escherichia						
P16518	bacterioph						
Q8x625	escherichia						
P09390	escherichia						
Q28029	bos taurus						
Q97950	clostridium						
O04350	arabidopsis						
Q41066	pisum sativ						
Q97949	saguinus oe						
P76172	escherichia						
P53300	saccharomyc						
O16864	homo sapien						
P50408	rattus norv						
P17724	tetrahymena						
Q03459	tetrahymena						
P73925	synechocyst						

691	19	82.6	124	1	YABJ_BACSU	P37552	19	82.6	160	1	ISPF_CORGL	Q8nmb9
692	19	82.6	124	1	YOB_A_ECOLI	P76279	19	82.6	160	1	ISPF_FUSNN	Q8-6e7
693	19	82.6	126	1	MSA_BORBU	P51339	19	82.6	160	1	R737_RICNN	Q8-6e7
694	19	82.6	127	1	FLIE_LEPIN	P81952	19	82.6	160	1	R737_RICPR	Q8-6e7
695	19	82.6	129	1	HMWR_RHILV	Q9x5v4	19	82.6	161	1	NAPB_PARPAN	Q8-6e7
696	19	82.6	129	1	VP14_BPAPS	Q9xtt4	19	82.6	161	1	T2DA_HUMAN	Q8-6e7
697	19	82.6	130	1	YRKG_CAEEL	Q914t4	19	82.6	162	1	ISPF_HERPE	Q8-6e7
698	19	82.6	139	1	DH1_HORVU	P12951	19	82.6	162	1	RIFK_HUMAN	Q8-6e7
699	19	82.6	139	1	FOB2_STAEP	Q03377	19	82.6	162	1	CDNA_FELCA	Q8-6e7
700	19	82.6	140	1	ATPE_NEIMA	Q91w69	19	82.6	164	1	T2DA_XENIA	Q8-6e7
701	19	82.6	140	1	ATPE_NEIMA	Q91w69	19	82.6	164	1	T2DA_XENIA	Q8-6e7
702	19	82.6	141	1	NUSB_NEIMA	Q91vd5	19	82.6	165	1	NUSB_PESNM	Q8-6e7
703	19	82.6	141	1	NUSB_NEIMA	Q91vd5	19	82.6	165	1	NUSB_PESNM	Q8-6e7
704	19	82.6	141	1	YV2_DHV11	Q01480	19	82.6	166	1	LUXS_HAEIN	Q8-6e7
705	19	82.6	141	1	ZURR_LISMO	Q01480	19	82.6	166	1	LUXS_HAEIN	Q8-6e7
706	19	82.6	142	1	FOB1_STAEP	P52921	19	82.6	166	1	NUSB_PSEPK	Q8-6e7
707	19	82.6	143	1	SILE_SALTY	P094n3	19	82.6	166	1	NUSB_PSEPK	Q8-6e7
708	19	82.6	146	1	HBB_ALIMI	P02130	19	82.6	167	1	YHGC_BACSU	Q8-6e7
709	19	82.6	147	1	TPC_TODPA	Q9b1g0	19	82.6	168	1	NUSB_NITEU	Q8-6e7
710	19	82.6	147	1	NUSB_CHRVO	Q7bvf2	19	82.6	169	1	RRAA_RALSO	Q8-6e7
711	19	82.6	150	1	GLPA_HUMAN	P02724	19	82.6	169	1	Y224_METUA	Q8-6e7
712	19	82.6	150	1	YBP2_STRAU	P23714	19	82.6	170	1	YLAC_ECOLI	Q8-6e7
713	19	82.6	151	1	GLXB_CHITH	P02228	19	82.6	170	1	DEF2_XANCP	Q8-6e7
714	19	82.6	151	1	R13_METKA	Q8tvc1	19	82.6	172	1	ADKH_DROME	Q8-6e7
715	19	82.6	152	1	DEF_NIGBR	Q84258	19	82.6	172	1	ADKH_DROME	Q8-6e7
716	19	82.6	152	1	I1FA_MOUSE	Q8-459	19	82.6	175	1	IF3_THEMA	Q8-6e7
717	19	82.6	152	1	RUVK_BIFLO	Q8-459	19	82.6	175	1	IF3_THEMA	Q8-6e7
718	19	82.6	153	1	IP2K_SOLTU	Q85x0	19	82.6	176	1	YV1_CAEEL	Q8-6e7
719	19	82.6	154	1	IP27_SOLTU	P01080	19	82.6	176	1	YV1_CAEEL	Q8-6e7
720	19	82.6	154	1	MRAZ_MYCPU	Q43652	19	82.6	181	1	ORN_VIBVU	Q8-6e7
721	19	82.6	155	1	ISPF_CLOAB	Q98g74	19	82.6	185	1	LGUL_BRAJU	Q8-6e7
722	19	82.6	155	1	RIFK_MOUSE	Q971x0	19	82.6	188	1	NRFB_ECOLI	Q8-6e7
723	19	82.6	155	1	R7B_BACST	Q8cfv9	19	82.6	189	1	APCD_RABIT	Q8-6e7
724	19	82.6	155	1	R7B_BACST	Q8cfv9	19	82.6	190	1	YV2_HUMAN	Q8-6e7
725	19	82.6	155	1	R7B_BACST	Q8cfv9	19	82.6	190	1	YV2_HUMAN	Q8-6e7
726	19	82.6	155	1	R7B_BACST	Q8cfv9	19	82.6	192	1	YV2_HUMAN	Q8-6e7
727	19	82.6	155	1	R7B_BACST	Q8cfv9	19	82.6	192	1	YV2_HUMAN	Q8-6e7
728	19	82.6	155	1	R7B_BACST	Q8cfv9	19	82.6	192	1	YV2_HUMAN	Q8-6e7
729	19	82.6	155	1	R7B_BACST	Q8cfv9	19	82.6	192	1	YV2_HUMAN	Q8-6e7
730	19	82.6	155	1	R7B_BACST	Q8cfv9	19	82.6	192	1	YV2_HUMAN	Q8-6e7
731	19	82.6	155	1	R7B_BACST	Q8cfv9	19	82.6	192	1	YV2_HUMAN	Q8-6e7
732	19	82.6	155	1	R7B_BACST	Q8cfv9	19	82.6	192	1	YV2_HUMAN	Q8-6e7
733	19	82.6	155	1	R7B_BACST	Q8cfv9	19	82.6	192	1	YV2_HUMAN	Q8-6e7
734	19	82.6	155	1	R7B_BACST	Q8cfv9	19	82.6	192	1	YV2_HUMAN	Q8-6e7
735	19	82.6	156	1	ATPF_VIBCH	P47334	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
736	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
737	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
738	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
739	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
740	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
741	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
742	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
743	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
744	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
745	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
746	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
747	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
748	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
749	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
750	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
751	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
752	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
753	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
754	19	82.6	156	1	ISPF_CLOPE	P30764	19	82.6	196	1	YCAK_ECOLI	Q8-6e7
755	19	82.6	157	1	ISPF_LISIN	Q92gh3	19	82.6	205	1	HYFA_ECOLI	Q8-6e7
756	19	82.6	157	1	ISPF_LISIN	Q92gh3	19	82.6	205	1	HYFA_ECOLI	Q8-6e7
757	19	82.6	157	1	ISPF_LISIN	Q92gh3	19	82.6	205	1	HYFA_ECOLI	Q8-6e7
758	19	82.6	157	1	ISPF_LISIN	Q92gh3	19	82.6	205	1	HYFA_ECOLI	Q8-6e7
759	19	82.6	157	1	ISPF_LISIN	Q92gh3	19	82.6	205	1	HYFA_ECOLI	Q8-6e7
760	19	82.6	158	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
761	19	82.6	158	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
762	19	82.6	158	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
763	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
764	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
765	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
766	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
767	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
768	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
769	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
770	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
771	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
772	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
773	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
774	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
775	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
776	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
777	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
778	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
779	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
780	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
781	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
782	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
783	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
784	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
785	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
786	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
787	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
788	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
789	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
790	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
791	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
792	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
793	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
794	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
795	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
796	19	82.6	159	1	ISPF_VIBPA	Q87lq3	19	82.6	206	1	YIM7_YEAST	Q8-6e7
797	19	82.6	159	1	ISPF_VIBPA	Q87lq						

837	19	82.6	227	1	6PGL_HELPY	O25730 helicobacte	910	19	82.6	288	1	PHZ2_MOUSE	Q9dc96 mus musculu
838	19	82.6	227	1	MAA2_DROME	Q9vhd3 drosophila	911	19	82.6	288	1	ZIPA_PSESM	Q87YV5 pseudomonas
839	19	82.6	227	1	MAD_MOUSE	P50538 mus musculu	912	19	82.6	294	1	YGAH_ECOLI	P25897 escherichia
840	19	82.6	227	1	NAPC_RHOSH	Q53178 rhodobacter	913	19	82.6	295	1	PNMT_MOUSE	P40935 mus musculu
841	19	82.6	228	1	RL1_THETH	P27150 thermus the	914	19	82.6	296	1	END4_STAEP	Q8cp25 staphylococ
842	19	82.6	230	1	FLAH_METVO	O06641 methanococ	915	19	82.6	297	1	ZIPA_PSEPK	Q88f24 pseudomonas
843	19	82.6	232	1	PYRE_SORMA	P18904 sordaria ma	916	19	82.6	298	1	PYRF_USTMA	P11188 ustilago ma
844	19	82.6	233	1	HIS9_THEMEA	Q9wzr1 thermotoga	917	19	82.6	299	1	BPHC_PSEPA	P11122 pseudomonas
845	19	82.6	233	1	OP67_NEIGO	Q05034 neisseria g	918	19	82.6	299	1	HEM6_ECO57	Q8xb14 escherichia
846	19	82.6	234	1	YVEK_BACSU	P71050 bacillus su	919	19	82.6	299	1	HEM6_ECOL6	Q8ffa3 escherichia
847	19	82.6	236	1	IPTI_AGRVI	Q04590 agrobacteri	920	19	82.6	299	1	HEM6_ECOLI	P36553 escherichia
848	19	82.6	236	1	YJ26_YEAST	P47115 saccharomyc	921	19	82.6	299	1	HYPB_RHILV	P28155 rhizobium l
849	19	82.6	237	1	NAPC_PARPEN	Q56352 paracoccus	922	19	82.6	300	1	SPSY_YEAST	Q12455 saccharomyc
850	19	82.6	237	1	Y913_BACHD	Q9ked9 bacillus ha	923	19	82.6	302	1	NAHC_PSEAE	Q57145 pseudomonas
851	19	82.6	237	1	YG6C_ECOLI	P11664 escherichia	924	19	82.6	303	1	HYPB_AZOV1	P31880 azotobacter
852	19	82.6	238	1	OP66_NEIGO	Q05033 neisseria g	925	19	82.6	305	1	HYPB_AZOCB	Q43949 azotobacter
853	19	82.6	238	1	RBP_CHICK	P02752 gallus gall	926	19	82.6	305	1	YG5T_YEAST	P53332 saccharomyc
854	19	82.6	239	1	DCUR_ECOL6	P59338 escherichia	927	19	82.6	306	1	ARGC_DEIRA	Q9ry72 deinococcus
855	19	82.6	239	1	DCUR_ECOLI	P39271 escherichia	928	19	82.6	308	1	CFA2_MYCLE	Q49807 mycobacteri
856	19	82.6	239	1	DCUR_SHIFL	P59339 shigella fl	929	19	82.6	308	1	GLS2_SALTY	Q8zp12 salmonella
857	19	82.6	244	1	CYSH_PHOLL	Q7mb85 photorhabdu	930	19	82.6	308	1	OPPF_STEMU	P72479 streptococc
858	19	82.6	244	1	RS2_BACHD	Q9ka63 bacillus ha	931	19	82.6	309	1	PLD_ARCHA	Q59121 arcanobacte
859	19	82.6	245	1	YGZA_YEAST	P53060 saccharomyc	932	19	82.6	310	1	SC65_YARLI	P41922 yarrowia li
860	19	82.6	247	1	FABG_MYCTU	Q48930 mycobacteri	933	19	82.6	310	1	VE2_HPV56	P36798 human papil
861	19	82.6	247	1	GRAN_GVAS	P31035 agrotis seg	934	19	82.6	310	1	YF85_METJA	Q58980 methanococc
862	19	82.6	248	1	WCAE_ECOLI	P71239 escherichia	935	19	82.6	311	1	OYJ3_HUMAN	Q8nh60 homo sapien
863	19	82.6	249	1	RT1D_MOUSE	Q9ji58 mus musculu	936	19	82.6	311	1	TXTP_BOVIN	P79110 bos taurus
864	19	82.6	251	1	RT1E_MOUSE	Q9czq6 mus musculu	937	19	82.6	311	1	TXTP_HUMAN	P53007 homo sapien
865	19	82.6	252	1	TPIS_NITEU	Q82tul nitrosomona	938	19	82.6	311	1	TXTP_RAT	P32089 rattus norv
866	19	82.6	253	1	CYSZ_SHIFL	Q83gm8 shigella fl	939	19	82.6	312	1	1A1D_THEMEA	Q9wy68 thermotoga
867	19	82.6	253	1	GLBL_TYLHE	P18207 tylosirynch	940	19	82.6	312	1	RIR2_R5TV	Q9qtf2 red sea bre
868	19	82.6	253	1	RT1A_MOUSE	O08602 mus musculu	941	19	82.6	314	1	MER2_YEAST	P12651 saccharomyc
869	19	82.6	253	1	RT1B_MOUSE	O08603 mus musculu	942	19	82.6	314	1	REP_LACHI	P35857 lactobacill
870	19	82.6	253	1	RT1C_MOUSE	O08604 mus musculu	943	19	82.6	314	1	YDQC_SCHPO	Q14204 schizosacch
871	19	82.6	253	1	SURE_ECOLI	P36664 escherichia	944	19	82.6	316	1	T2R3_HUMAN	Q9nyw6 homo sapien
872	19	82.6	253	1	SURE_SHIFL	Q83jy2 shigella fl	945	19	82.6	316	1	Y3SK_HALSG	P17565 halobacteri
873	19	82.6	254	1	ETFB_SCHPO	Q9uth2 schizosacch	946	19	82.6	317	1	PECR_ECOLI	P23485 escherichia
874	19	82.6	254	1	RS2_OETH	O8egv3 oceanobacil	947	19	82.6	317	1	YVCK_BACSU	O06974 bacillus su
875	19	82.6	255	1	FABG_MYCAV	O07399 mycobacteri	948	19	82.6	319	1	COAA_BACSU	P54556 bacillus su
876	19	82.6	255	1	FABG_MYCSM	P71534 mycobacteri	949	19	82.6	320	1	CYF_WARPO	P06246 marchantia
877	19	82.6	255	1	FOLI_MOUSE	P35846 mus musculu	950	19	82.6	321	1	MRAW_HAFIN	P45057 haemophilus
878	19	82.6	255	1	GAG_IPMAE	P31790 mouse intra	951	19	82.6	322	1	Y486_METJA	Q57910 methanococc
879	19	82.6	256	1	YAFV_ECOLI	Q47679 escherichia	952	19	82.6	323	1	CDC2_EMENI	O06646 emericella
880	19	82.6	257	1	FOLI_HUMAN	P15328 homo sapien	953	19	82.6	323	1	CITG_HARDU	Q30827 haemophilus
881	19	82.6	257	1	NOCP_AGRTS	P35116 agrobacteri	954	19	82.6	323	1	LUKF_STAAR	P31715 staphylococ
882	19	82.6	260	1	HIS9_DEIRA	Q9rx45 deinococcus	955	19	82.6	324	1	ANXA_HUMAN	Q9uj72 homo sapien
883	19	82.6	261	1	TATD_ECOLI	P27859 escherichia	956	19	82.6	324	1	ANXA_MOUSE	Q9qz10 mus musculu
884	19	82.6	261	1	KLK1_RAT	P00758 rattus norv	957	19	82.6	324	1	CDC2_AJECA	P54119 ajelloymyces
885	19	82.6	262	1	RS2_ENTFA	Q831u9 enterococcu	958	19	82.6	325	1	BLA1_STRCI	Q03680 streptomyces
886	19	82.6	262	1	YU09_MYCGE	P47255 mycoplasma	959	19	82.6	325	1	HLGB_STAAN	Q07226 staphylococ
887	19	82.6	262	1	YU48_ENTFA	P59745 enterococcu	960	19	82.6	325	1	TOLC_BACSU	P42414 bacillus su
888	19	82.6	263	1	YH25_DEIRA	O83030 deinococcus	961	19	82.6	327	1	K6PF_SPCIC	P20275 spiroplasma
889	19	82.6	265	1	DCMR_METSP	P45876 methylobact	962	19	82.6	329	1	G3P_KLUJA	P17819 kluyveromyc
890	19	82.6	268	1	HIS9_BACSU	Q34411 bacillus su	963	19	82.6	329	1	SQV7_CAEEL	P18779 caenorhabd
891	19	82.6	272	1	RS2_CORGL	Q8np01 corynebacte	964	19	82.6	331	1	G3P2_YEAST	P00358 saccharomyc
892	19	82.6	272	1	VAL1_MSVK	O01568 maize strea	965	19	82.6	331	1	G3P_CANAL	Q92211 candida alb
893	19	82.6	272	1	VAL1_MSVN	P14980 maize strea	966	19	82.6	331	1	LDHA_MONDO	Q9xt87 monodelphis
894	19	82.6	272	1	VAL1_MSVS	P14990 maize strea	967	19	82.6	331	1	LDHA_SEEUN	Q9w715 sceloporius
895	19	82.6	273	1	HIS9_BACHD	Q9k801 bacillus ha	968	19	82.6	332	1	DUSA_PSEAE	Q91048 pseudomonas
896	19	82.6	273	1	PRXC_PSEFL	Q31158 pseudomonas	969	19	82.6	332	1	LDHA_RAT	P04642 rattus norv
897	19	82.6	274	1	NADE_LISIN	Q92cu3 listeria in	970	19	82.6	332	1	YC56_PASMU	Q9clh5 pasteurella
898	19	82.6	274	1	NADE_LISMO	Q8y825 listeria mo	971	19	82.6	332	1	YIAK_HARIN	P44995 haemophilus
899	19	82.6	275	1	HPCB_ECOLI	Q05353 escherichia	972	19	82.6	333	1	LDHB_BRARE	Q9pvk4 brachydanio
900	19	82.6	275	1	NADE_STAEP	Q8cnpl staphylococ	973	19	82.6	334	1	ILVC_METJA	Q58938 methanococc
901	19	82.6	275	1	YCT7_YEAST	P25627 saccharomyc	974	19	82.6	334	1	LDHB_STAAC	Q9y105 aqualus aca
902	19	82.6	276	1	RS2_COREF	Q8fp70 corynebacte	975	19	82.6	335	1	LPXK_VIBUO	Q8davi vibrio vuln
903	19	82.6	281	1	PANB_MYCTU	O10505 mycobacteri	976	19	82.6	335	1	STXH_HUMAN	Q9p2w3 homo sapien
904	19	82.6	281	1	PANC_CLOBR	Q97f38 clostridium	977	19	82.6	336	1	LDHD_LACHE	P30901 lactobacill
905	19	82.6	285	1	OPF3_NPOVP	P90212 oryza pseeu	978	19	82.6	336	1	YERT_BACSU	Q34640 bacillus su
906	19	82.6	285	1	PNMT_RAT	P10937 rattus norv	979	19	82.6	337	1	G3PI_AGABI	P32635 agaricus bi
907	19	82.6	287	1	RP32_BUCBP	Q89b27 buchnera ap	980	19	82.6	338	1	RL3_HALMA	P20279 haloarcula
908	19	82.6	287	1	SYGA_CAMJE	Q9ppk3 campylobact	981	19	82.6	339	1	ILVC_BRUME	Q8y121 brucella me
909	19	82.6	288	1	PHZ1_MOUSE	Q9cxn7 mus musculu	982	19	82.6	339	1	ILVC_BRUSU	Q8fzu1 brucella su

983 19 82.6 340 1 GLSA\_YERPE  
 984 19 82.6 341 1 PAFR\_MOUSE  
 985 19 82.6 341 1 PAFR\_RAT  
 986 19 82.6 342 1 ILVC\_BACSU  
 987 19 82.6 342 1 PAFR\_CAVPO  
 988 19 82.6 342 1 PAFR\_HUMAN  
 989 19 82.6 344 1 HMD\_METTF  
 990 19 82.6 344 1 HMD\_METTH  
 991 19 82.6 344 1 HMD\_METTW  
 992 19 82.6 344 1 HMD\_METTW  
 993 19 82.6 344 1 RPF2\_YEAST  
 994 19 82.6 345 1 OGG1\_HUMAN  
 995 19 82.6 345 1 OGG1\_MOUSE  
 996 19 82.6 345 1 OGG1\_RAT  
 997 19 82.6 345 1 OUEA\_HELPJ  
 998 19 82.6 345 1 OUEA\_HELPY  
 999 19 82.6 346 1 TRAJ\_LEPPO  
 1000 19 82.6 347 1 HDL1\_HUMAN

## ALIGNMENTS

RESULT 1  
 PTLA\_STRMU STANDARD; PRT; 104 AA.  
 AC P26426;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE PTS system, lactose-specific IIA component (EIIA-LAC) (Lactose-  
 permease IIA component) (Phosphotransferase enzyme II, A component)  
 DE (EC 2.7.1.69) (EIII-LAC).  
 GN LACF OR SMU.1492.  
 OS Streptococcus mutans.  
 CC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;  
 CC Streptococcus.  
 CC NCBI\_TaxID=11309;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93015655; PubMed=1400164;  
 RA Rosey E.L., Stewart G.C.;  
 RT "Nucleotide and deduced amino acid sequences of the lacR, lacABCD,  
 RT and lacFE genes encoding the repressor, tagatose 6-phosphate gene  
 RT cluster, and sugar-specific phosphotransferase system components of  
 RT the lactose operon of Streptococcus mutans.";  
 RL J. Bacteriol. 174:6159-6170(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=UA159 / ATCC 700610 / Serotype C;  
 RX MEDLINE=22295063; PubMed=12397186;  
 RA Ajdic D., McShan W.M., McLaughlin R.E., Savic G., Chang J., Qian Y.,  
 RA Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S., Jia Y.,  
 RA Li S., Zhu H., Najjar F., Lai H., White J., Roe B.A., Ferretti J.J.;  
 RT "Genome sequence of Streptococcus mutans UA159, a cariogenic dental  
 RT pathogen.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14434-14439(2002).  
 CC -!- FUNCTION: This is a component of the phosphoenolpyruvate-dependent  
 CC sugar phosphotransferase system (PTS), a major carbohydrate active  
 CC -transport system. The IID domains contain the sugar binding site  
 CC and the transmembrane channel; the IIA domain contains the primary  
 CC phosphorylation site (the donor is phospho-HPr); IIA transfers its  
 CC phosphoryl group to the IIB domain which finally transfers it to  
 CC the sugar.  
 CC -!- CATALYTIC ACTIVITY: Protein N-phosphohistidine + sugar = protein  
 CC histidine + sugar phosphate.  
 CC -!- COFACTOR: Binds 1 magnesium or manganese ion per trimer (By  
 CC similarity).  
 CC -!- SUBUNIT: Homotrimer.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Contains 1 PTS EIIA domain.  
 CC -----  
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 CC -----  
 DR EMBL; M80797; AAA26908.1; -;  
 DR EMBL; AE014981; AAN59146.1; -;  
 DR PIR; G43258; G43258.  
 DR HSSP; P23532; 1E2A.  
 DR InterPro; IPR003188; Ptrans IIA.  
 DR Pfam; PF02255; PTS IIA; 1.  
 DR ProDom; PD007286; PTS IIA; 1.  
 DR TIGRFAMs; TIGR00823; EIIA-LAC; 1.  
 KW Phosphotransferase system; Sugar transport; Transferase;  
 KW Phosphorylation; Metal-binding; Magnesium; Manganese;  
 KW Complete proteome.  
 FT METAL 81  
 FT MOD RES 78 78  
 SQ SEQUENCE 104 AA; 11399 MW; 281CB2F3CB109F5D CRC64;

Query Match 100.0%; Score 23; DB 1; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 42;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAKH 4  
 ||||  
 DB 52 DAKH 55

RESULT 2  
 Y210\_COREF  
 ID\_Y210\_COREF STANDARD; PRT; 107 AA.  
 AC Q8FVU1;  
 DT 10-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hypothetical UPF0133 protein CE0210.  
 GN CE0210.  
 OS Corynebacterium efficiens.  
 CC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 CC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
 CC NCBI\_TaxID=152794;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;  
 RX MEDLINE=22723752; PubMed=12840036;  
 RA Nishio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,  
 RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,  
 RA Gojobori T.;  
 RT "Comparative complete genome sequence analysis of the amino acid  
 RT replacements responsible for the thermostability of Corynebacterium  
 RT efficiens.";  
 RL Genome Res. 13:1572-1579(2003).  
 CC -!- SUBUNIT: Homodimer (By similarity).  
 CC -!- SIMILARITY: Belongs to the UPF0133 family.  
 CC -----  
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 CC -----  
 DR EMBL; AP005214; BAC17020.1; ALT\_INIT.  
 DR HAMAP; MF\_00274; -; 1.  
 DR InterPro; IPR004401; Cons\_hypoth103.  
 DR Pfam; PF02575; DUF149; 1.  
 DR TIGRFAMs; TIGR00103; TIGR00103; 1.  
 KW Hypothetical protein; Complete proteome  
 SQ SEQUENCE 107 AA; 11160 MW; 288F22C385CAC6B8 CRC64;



Query Match 100.0%; Score 23; DB 1; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 43;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 DB 79 DAHK 82

## RESULT 3

RBFA\_UREPA STANDARD; PRT; 116 AA.  
 AC QPQHO; 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DE 28-FEB-2003 (Rel. 41, Last annotation update)  
 DR Ribosome-binding factor A.  
 GN RBFA OR U0321.

OS Ureaplasma parvum (Ureaplasma urealyticum biotype 1).  
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.  
 OX NCBI\_TaxID=134821;  
 RN [1]  
 RC STRAIN=Serovar 3;  
 RX MEDLINE=20500219; PubMed=11048724;  
 RA Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y.,  
 Cassell G.H.;

RT "The complete sequence of the mucosal pathogen Ureaplasma

urealyticum.";

RL Nature 407:757-762 (2000).

CC -!- FUNCTION: Associates with free 30S ribosomal subunits (but not  
 with 30S subunits that are part of 70S ribosomes or polysomes).  
 Essential for efficient processing of 16S rRNA. May interact with  
 the 5' terminal helix region of 16S rRNA (By similarity).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).

CC -!- SIMILARITY: Belongs to the rbfA family.

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CC -----

CC EMBL; AE002129; AAF30730.1; -.

DR HAMAP; MF 00003; -; 1.

DR InterPro; IPR000238; Rib\_bind\_facta.

DR Pfam; PF02033; RBFA; 1.

DR ProDom; PD007327; Rib\_bind\_facta; 1.

DR TIGRFAMs; TIGR00082; rbfA; 1.

DR PROSITE; PS01319; RBFA; FALSE NEG.

KW rRNA processing; Complete proteome.

SQ SEQUENCE 116 AA; 13247 MW; A79DCC71F0547514 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 DB 53 DAHK 56

## RESULT 4

HBB\_RANES STANDARD; PRT; 140 AA.  
 AC P02134;  
 DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hemoglobin beta chain.

GN HBB.  
 OS Rana esculenta (Edible frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranae;  
 OX NCBI\_TaxID=8401;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72111329; PubMed=4536743;  
 RA Chauvet J.-P., Acher R.;  
 RT "Phylogeny of hemoglobins. Beta chain of frog (*Rana esculenta*)  
 hemoglobin.";  
 RL Biochemistry 11:916-927 (1972).  
 CC -!- FUNCTION: Involved in oxygen transport from the lung to the  
 various peripheral tissues.  
 CC -!- SUBUNIT: Heterotetramer of two alpha chains and two beta chains.  
 CC -!- TISSUE SPECIFICITY: Red blood cells.  
 CC -!- SIMILARITY: Belongs to the globin family.

DR PIR; A02454; HBBGRE.

DR HSSP; P02023; 1BAB.

DR InterPro; IPR002337; Beta haem.

DR InterPro; IPR000971; Globin.

DR Pfam; PF00042; globin; 1.

DR PRINTS; PR00814; BETAHAEM.

DR PROSITE; PS01033; GLOBIN; 1.

KW Heme; Oxygen transport; Transport; Erythrocyte.

FT METAL 57 57 IRON (HEME DISTAL LIGAND).

FT METAL 91 91 IRON (HEME PROXIMAL LIGAND).

SQ SEQUENCE 140 AA; 15423 MW; 151F75CF7076AAB0 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 140;

Best Local Similarity 100.0%; Pred. No. 57;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4

DB 13 DAHK 16

## RESULT 5

FUR\_VIBPA

ID FUR\_VIBPA STANDARD; PRT; 149 AA.

AC O24755;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ferric uptake regulation protein (ferric uptake regulator).

GN FUR OR VP0833.

OS Vibrio parahaemolyticus.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;

OC Vibrionaceae; Vibrio.

OX NCBI\_TaxID=670;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=RIMD WPI;

RX MEDLINE=98003754; PubMed=9343826;

RA Yamamoto S., Funahashi T., Ikai F., Shinoda S.;

RT "Cloning and sequencing of the Vibrio parahaemolyticus fur gene.";

RL Microbiol. Immunol. 41:737-740 (1997).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=RIMD 2210633 / Serotype O3:K6;

RX MEDLINE=22508454; PubMed=12620739;

RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.;

RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.;

RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism

distinct from that of *V. cholerae*.";

RL Lancet 361:743-749 (2003).

CC -!- FUNCTION: FUR ACTS AS A REPRESSOR, EMPLOYING FE(2+) AS A COFACTOR

TO BIND THE OPERATOR OF THE IRON TRANSPORT OPERON.

CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

CC -!- SIMILARITY: Belongs to the Fur family.

CC -----



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DR EMBL; AB003752; BAA22785.1; -;  
 DR EMBL; AP005075; BAC59096.1; -;  
 DR InterPro: IPR002481; FUR.  
 DR Pfam; PF01475; FUR; 1.  
 DR ProDom; P0002003; FUR; 1.  
 KW Transcription regulation; Repressor; DNA-binding; Iron; Zinc;  
 KW Complete proteome.  
 FT DOMAIN 86 HIS-RICH.  
 FT METAL 93 ZINC (BY SIMILARITY).  
 FT METAL 96 ZINC (BY SIMILARITY).  
 SQ SEQUENCE 149 AA; 16771 MW; 72E66238380D36BD CRC64;

Query Match 100.0%; Score 23; DB 1; Length 149;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 Db 143 DAHK 146

## RESULT 6

FUR\_VIBVU STANDARD; PRT; 149 AA.  
 AC P33117;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ferric uptake regulation protein (ferric uptake regulator).  
 FUR OR VVI0175.  
 OS Vibrio vulnificus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; Vibrio.  
 OX NCBI\_TaxID=672;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93139039; PubMed=7678593;  
 RA Litwin C.M., Calderwood S.B.;  
 RA "Cloning and genetic analysis of the *Vibrio vulnificus* fur gene and  
 RT construction of a fur mutant by in vivo marker exchange."  
 RL J. Bacteriol. 175:706-715(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CMCP6;  
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
 RA Choy H.E.;  
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6."  
 RL Submitted (DSC-2002) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: FUR ACTS AS A REPRESSOR, EMPLOYING FE(2+) AS A COFACTOR  
 CC TO BIND THE OPERATOR OF THE IRON TRANSPORT OPERON.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -!- SIMILARITY: Belongs to the Fur family.  
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DR EMBL; L06428; AAA27521.1; -;  
 DR EMBL; AE016797; AAO08713.1; -;  
 DR PIR; A47054; A47054.  
 DR InterPro: IPR002481; FUR.

DR Pfam; PF01475; FUR; 1.  
 DR ProDom; P0002003; FUR; 1.  
 KW Transcription regulation; Repressor; DNA-binding; Iron; Zinc;  
 KW Complete proteome.  
 FT DOMAIN 86 HIS-RICH.  
 FT METAL 93 ZINC (BY SIMILARITY).  
 FT METAL 96 ZINC (BY SIMILARITY).  
 FT CONFLICT 149 N -> S (IN REF. 1).  
 SQ SEQUENCE 149 AA; 16743 MW; 3C54EBB82C0F21C8 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 149;  
 Best Local Similarity 100.0%; Pred. No. 61;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
 Db 143 DAHK 146

## RESULT 7

HUTP\_BACSU STANDARD; PRT; 151 AA.  
 AC P10943;  
 DT 01-JUL-1989 (Rel. 11, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Hut operon positive regulatory protein.  
 GN HUTP OR BSU3340.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8257040; PubMed=2454913;  
 RA Oda M., Sugishita A., Furukawa K.;  
 RA "Cloning and nucleotide sequences of histidase and regulatory genes  
 RT in the *Bacillus subtilis* hut operon and positive regulation of the  
 RL operon."  
 RL J. Bacteriol. 170:3199-3205(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168 / BGSC1A1;  
 RX MEDLINE=95219088; PubMed=7704263;  
 RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;  
 RA "Cloning and sequencing of a 29 kb region of the *Bacillus subtilis*  
 RT genome containing the hut and wpa loci."  
 RL Microbiology 141:337-343(1995).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=98044033; PubMed=9384377;

RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,  
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borcherdt S.,  
 RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,  
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D., N.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,  
 RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,  
 RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,  
 RA Medina N., Mellado R.P., Mizuno M., Mostl D., Nakai S., Noback M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,  
 RA Presecan E., Pujić P., Purnelle B., Rapoport G., Rey M., Reynolds S.,  
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,  
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,  
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,  
 RA Winters P., Wipat A., Yamamoto H., Yanane K., Yasumoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,  
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*  
 RT *subtilis*,"  
 RL Nature 390:249-256 (1997).  
 CC -!- FUNCTION: POSITIVE REGULATOR OF THE HISTIDINE UTILIZATION (HUT)  
 CC OPERON.  
 CC -----  
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 CC -----  
 DR EMBL; M20659; AAA22537.1; -;  
 DR EMBL; D31856; BAA06645.1; -;  
 DR EMBL; Z99124; CAB15970.1; -;  
 DR PIR; S18809; RGSHP.  
 DR Subtilist; BG10666; hutP.  
 KW Histidine metabolism; Transcription regulation; Activator;  
 KW DNA-binding; Complete proteome.  
 SQ SEQUENCE 151 AA; 16577 MW; E27ABDA7A533C35D CRC64;  
 Query Match 100.0%; Score 23; DB 1; Length 151;  
 Best Local Similarity 100.0%; Pred. No. 62;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAHK 4  
 Db 49 DAHK 52  
 RESULT 8  
 ATPF\_VIBVU STANDARD; PRT; 156 AA.  
 ID ATPF\_VIBVU  
 AC Q8DDH2;  
 DT 15-MAR-2004 (Rel. 43, Created)  
 DT 15-MAR-2004 (Rel. 43, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE ATP synthase B chain (EC 3.6.3.14).  
 GN ATPF OR VW11017.  
 OS *Vibrio vulnificus*.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;  
 OC Vibrionaceae; *Vibrio*.  
 OX NCBI\_TaxID=672;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CMCP6;  
 RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,  
 RA Choy H.E.;  
 RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +  
 CC H(+) (Out).  
 CC -!- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic  
 CC core - and CF(0) - the membrane proton channel. CF(1) has five  
 CC subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)  
 CC has three main subunits: a, b and c (By similarity).  
 CC -!- SIMILARITY: Belongs to the ATPase B chain family.  
 CC -----  
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 CC -----

CC EMBL; AE016800; AAO09505.1; ALT INIT.  
 DR InterPro; IPR002146; ATPynt B/E' sub.  
 DR InterPro; IPR005864; ATP\_synthF0\_B.  
 DR Pfam; PF00430; ATP-synt\_B; 1.  
 DR TIGRFAMs; TIGR01144; ATP synt\_b; 1.  
 KW Hydrogen ion transport; Transmembrane; CF(0); Complete proteome.  
 FT TRANSMEM 2 22 POTENTIAL.  
 SQ SEQUENCE 156 AA; 17562 MW; 01FE27B4F037ALB0 CRC64;  
 Query Match 100.0%; Score 23; DB 1; Length 156;  
 Best Local Similarity 100.0%; Pred. No. 64;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 DAHK 4  
 Db 143 DAHK 146  
 RESULT 9  
 LCRH\_YERPE STANDARD; PRT; 168 AA.  
 ID LCRH\_YERPE  
 AC P21207;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Low calcium response locus protein H.  
 GN LCRH OR YPCD1.30C OR Y5048 OR Y0051.  
 OS *Yersinia pestis*.  
 OG Plasmid pCD1.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; *Yersinia*.  
 OX NCBI\_TaxID=632;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KIM5 / Biovar Mediaevalis;  
 RX MEDLINE=9000806; PubMed=2477361;  
 RA Price S.B., Leung K.Y., Barve S.S., Straley S.C.;  
 RT "Molecular analysis of lcrGVH, the V antigen operon of *Yersinia*  
 RT *pestis*,"  
 RL J. Bacteriol. 171:5646-5653 (1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KIM5 / Biovar Mediaevalis;  
 RX MEDLINE=98427122; PubMed=9746557;  
 RA Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,  
 RA Blattner F.R.;  
 RT "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of  
 RT *Yersinia pestis* KIM5,"  
 RL Infect. Immun. 66:4611-4623 (1998).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=KIM5 / Biovar Mediaevalis;  
 RX MEDLINE=98422474; PubMed=9748454;  
 RA Hu P., Elliott J., McCready P., Skowronski E., Garnes J.,  
 RA Kobayashi A., Brubaker R.R., Garcia E.;  
 RT "Structural organization of virulence-associated plasmids of *Yersinia*  
 RT *pestis*,"  
 RL J. Bacteriol. 180:5192-5202 (1998).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CO-92 / Biovar Orientalis;  
 RX MEDLINE=21470413; PubMed=11586360;  
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,  
 RA Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,  
 RA Baker S., Basham D., Bentley S.D., Davies R.M., Davis P., Dougan G.,  
 RA Chillingworth T., Cronin A., Holroyd S., Jagels K., Karlyshev A.V.,  
 RA Feltwell T., Hamlin N., Holroyd S., Quail M.A., Rutherford K.,  
 RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,  
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;  
 RT "Genome sequence of *Yersinia pestis*, the causative agent of plague,"  
 RL Nature 413:523-527 (2001).  
 CC -!- FUNCTION: MEDIATES THE NEGATIVE REGULATION OF THE LCRGVH OPERON BY

ATP OR CA(2+). ACTS AS A MODULATOR OF THE YOP OPERON EXPRESSION.  
 -!- SIMILARITY: TO SHIGELLA INVASION PLASMID IPPI PROTEIN.

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-----  
 EMBL; M26405; AAC27642.1; -.  
 EMBL; AF074612; AAC69800.1; -.  
 EMBL; AF053946; AAC62575.1; -.  
 EMBL; AL117189; CAB54907.1; -.  
 PIR; C33601; C33601.  
 InterPro; IPR008940; Prenyl\_trans.  
 InterPro; IPR005415; SycD\_chap.  
 InterPro; IPR001440; TPR.  
 PRINTS; PR01595; SYCDCHAPRONE.  
 Plasmid; Complete proteome.  
 SQ SEQUENCE 168 AA; 19014 MW; 46206AF240EB0064 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 DB 54 DAHK 57

RESULT 10  
 LCRH YERPS STANDARD; PRT; 168 AA.  
 AC P23995;  
 DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE Low calcium response locus protein H.  
 GN LCRH.  
 OS Yersinia pseudotuberculosis.  
 OG Plasmid pIB1.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Yersinia.  
 OX NCBI\_TaxID=633;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=YPIII;  
 RX MEDLINE=91154114; PubMed=1705541;  
 RA Bergman T., Haakanson S., Forsberg A., Norlander L., Macellaro A., Baeckman A., Boelin I., Wolf-Watz H.;  
 RT "Analysis of the V antigen *lcrGVH-yopBD* operon of *Yersinia pseudotuberculosis*: evidence for a regulatory role of *LcrH* and *LcrV*.";  
 RT *J. Bacteriol.* 173:1607-1616(1991).  
 RL J. Bacteriol. 173:1607-1616(1991).  
 CC -!- FUNCTION: MEDIATES THE NEGATIVE REGULATION OF THE LCRGVH OPERON BY ATP OR CA(2+). ACTS AS A MODULATOR OF THE YOP OPERON EXPRESSION.  
 CC -!- SIMILARITY: TO SHIGELLA INVASION PLASMID IPPI PROTEIN.

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 EMBL; M57893; AAA27646.1; -.  
 PIR; C37314; C37314.  
 InterPro; IPR008940; Prenyl\_trans.  
 InterPro; IPR005415; SycD\_chap.  
 InterPro; IPR001440; TPR.

DR PRINTS; PR01595; SYCDCHAPRONE.  
 KW Plasmid.  
 SQ SEQUENCE 168 AA; 19010 MW; 2CE06AF240EB0424 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 168;  
 Best Local Similarity 100.0%; Pred. No. 69;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 DB 54 DAHK 57

RESULT 11  
 PHAF CYACA STANDARD; PRT; 170 AA.  
 ID PHAF CYACA  
 AC O19896;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Allophycocyanin beta 18 chain.  
 GN APCF.  
 OS Cyanidium caldarium.  
 OG Chloroplast.  
 OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;  
 OC Cyanidium.  
 OX NCBI\_TaxID=2771;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=RK-1;  
 RX MEDLINE=20496959; PubMed=11040290;  
 RA Gloeckner G., Rosenthal A., Valentin K.-U.;  
 RT "The structure and gene repertoire of an ancient red algal plastid genome.";  
 RL *J. Mol. Evol.* 51:382-390(2000).  
 CC -!- FUNCTION: Light-harvesting photosynthetic bile pigment-protein from the phycobiliprotein complex. Allophycocyanin has a maximum absorption at approximately 650 nanometers.  
 CC -!- SUBUNIT: Heterodimer of an alpha and a beta chain.  
 CC -!- PTM: Contains one covalently linked bilin chromophore.

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 EMBL; AF022186; AAB82693.1; -.  
 PIR; T11964; T11964.  
 HSP; P00318; I833.  
 InterPro; IPR006245; ApcB.  
 InterPro; IPR001659; Phycobilisome.  
 Pfam; PF00502; Phycobilisome; 1.  
 ProDom; PD000340; Phycobilisome; 1.  
 TIGRfams; TIGR01337; apcB; 1.  
 DR Phycobilisome; Electron transport; Photosynthesis; Bile pigment;  
 KW Chloroplast; Methylation.  
 FT MOD RES 74 84  
 FT BINDING 84 84 METHYLATION (BY SIMILARITY).  
 FT PHYCOCYANOBILIN CHROMOPHORE (BY SIMILARITY).  
 SQ SEQUENCE 170 AA; 19231 MW; 24914859DC69B185 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 70;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 DB 149 DAHK 152

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RESULT 12
IPYR BRAJA STANDARD; PRT; 178 AA.
AC Q89WY0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
DE hydrolase) (PPase).
GN PPA OR BLR0548.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Iidesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Teurucka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
CC -!- COFACTOR: Binds 4 magnesium ions per subunit. Other metal ions can
CC support activity, but at a lower rate. Two magnesium ions are
CC required for the activation of the enzyme and are present before
CC substrate binds, two additional magnesium ions form complexes with
CC substrate and product (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the Ppase family.
CC
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CC
CC EMBL; AF005936; BAC45813.1; -.
CC HAMAP; MF_00209; -.
CC InterPro; IPR008163; Inorg_pphsp.
CC InterPro; IPR008162; Pyrophosphatase.
CC Pfam; PF00719; Pyrophosphatase; 1.
CC ProDom; PD002014; Inorg_pphsp; 1.
CC PROSITE; PS00387; PPASE; FALSE_NEG.
KW Hydrolase; Metal-binding; Magnesium; Complete proteome.
FT METAL 66 66 MAGNESIUM 1 (BY SIMILARITY).
FT METAL 71 71 MAGNESIUM 1 AND 2 (BY SIMILARITY).
FT METAL 103 103 MAGNESIUM 1 (BY SIMILARITY).
SQ SEQUENCE 178 AA; 20052 MW; EF8F8BDF15D51EB1 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4
Db 161 DAHK 164

RESULT 13
SODF_TETPY STANDARD; PRT; 196 AA.
AC P19666;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Fe] (EC 1.15.1.1).
OS Tetrahymena pyriformis.

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OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
OC Tetrahymenina; Tetrahymena.
OX NCBI_TaxID=5908;
RN [1]
RP SEQUENCE.
RX MEDLINE=91009226; PubMed=2170391;
RA Barra D., Schinina M.E., Bossa F., Puget K., Durosay P., Guissani A.,
RA Michelson A.M.;
RT "A tetrameric iron superoxide dismutase from the eucaryote
RT Tetrahymena pyriformis.";
RL J. Biol. Chem. 285:17680-17687(1990).
CC -!- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -!- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -!- SUBUNIT: Homotetramer.
CC -!- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC PIR; A39223; A39223.
DR HSSP; P04179; 1AP6.
DR InterPro; IPR001189; SODismutase.
DR Pfam; PF00081; sodfe; 1.
DR Pfam; PF02777; sodfe_C; 1.
DR PRINTS; PR01703; MNSODISMUTASE.
DR ProDom; PD000475; SODismutase; 1.
DR PROSITE; PS00088; SOD_MN; 1.
KW Oxidoreductase; Metal-binding; Iron.
FT METAL 20 20 IRON (BY SIMILARITY).
FT METAL 68 68 IRON (BY SIMILARITY).
FT METAL 157 157 IRON (BY SIMILARITY).
FT METAL 161 161 IRON (BY SIMILARITY).
SQ SEQUENCE 196 AA; 22657 MW; FC1P2F67893D8DC7 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4
Db 47 DAHK 50

RESULT 14
UBAL CANAL STANDARD; PRT; 205 AA.
ID UBAL CANAL
AC P52495;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ubiquitin-activating enzyme E1 1 (Fragment).
GN UBAL
OS Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WO-1;
RA Raymond M., Dignard D., Mainville N., Magee B.B., Thomas D.Y.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Activates ubiquitin by first adenylating with ATP its
CC carboxy-terminal glycine residue and thereafter linking this
CC residue to the side chain of a cysteine residue in E1, yielding an
CC ubiquitin-E1 thioester and free AMP (By similarity).
CC -!- PATHWAY: Ubiquitin conjugation; first step.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
CC -!- MISCELLANEOUS: There are two active sites within the E1 molecule,
CC allowing it to accommodate two ubiquitin moieties at a time, with a
CC new ubiquitin forming an adenylate intermediate as the previous
CC one is transferred to the thiol site (By similarity).
CC -!- SIMILARITY: Belongs to the ubiquitin-activating E1 family.
CC

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Job time : 45 s3cs

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CC -----

DR EMBL; U13193; AAC49911.1; --  
DR PIR; T18215; T18215.  
DR InterPro; IPR000127; UBact\_repeat.  
DR InterPro; IPR000011; Ugtin\_activ\_enz.  
DR Pfam; PF02134; UBACT; 1.  
DR PROSITE; PS00536; UBIQUITIN\_ACTIVAT\_1; PARTIAL.  
DR PROSITE; PS00865; UBIQUITIN\_ACTIVAT\_2; PARTIAL.  
KW Ubl conjugation pathway; Ligase.  
FT NON TER 1  
SQ SEQUENCE 205 AA; 23166 MW; CD3F5BA99D0D2697 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 205;  
Best Local Similarity 100.0%; Pred. No. 85;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAAK 4  
|  
|  
|  
|  
DB 32 DAAK 35

## RESULT 15

VG66\_BFMLS  
ID VG66\_BFMLS STANDARD; PRT; 207 AA.  
AC Q05280;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1994 (Rel. 28, Last sequence update)  
DT 01-FEB-1994 (Rel. 28, Last annotation update)  
DE Gene 66 protein (GF66).  
GN 66.  
OS Mycobacteriophage L5.  
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
OC L5-like viruses.  
OX NCBI\_TaxID=31757;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=93211282; PubMed=8459766;  
RA Hatfull G.F., Sarkis G.J.;  
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:  
RT a phage system for mycobacterial genetics.";  
RL Mol. Microbiol. 7:395-405(1993).  
CC -----

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CC -----

DR EMBL; Z18946; CAA79442.1; --  
DR PIR; S31011; S31011.  
DR InterPro; IPR004843; M-ppetrase.  
DR Pfam; PF00149; Metallophos; 1.  
SQ SEQUENCE 207 AA; 23581 MW; 668BF8C639C7B20C CRC64;

Query Match 100.0%; Score 23; DB 1; Length 207;  
Best Local Similarity 100.0%; Pred. No. 86;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAAK 4  
|  
|  
|  
|  
DB 92 DAAK 95

Search completed: September 9, 2004, 23:45:38

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OM protein - protein search, using sw model

Run on: September 9, 2004, 23:45:44 ; Search time 128 Seconds  
(without alignments)

10.022 Million cell updates/sec

Title: US-10-076-071-1

Perfect score: 23

Sequence: 1 DAKH 4

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Published Applications AA:\*

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pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	23	100.0	4	14	US-10-205-110-35
5	23	100.0	4	14	US-10-300-664-1
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7	23	100.0	5	12	US-10-436-549-422
8	23	100.0	5	14	US-10-205-110-42
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11	23	100.0	7	15	US-10-393-992-2
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15	23	100.0	10	10	US-09-572-404B-2522

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25	23	100.0	15	14	US-10-073-118-40	Sequence 40, Appl
26	23	100.0	17	9	US-09-845-727-1	Sequence 1, Appl
27	23	100.0	24	9	US-09-846-328-1	Sequence 1, Appl
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32	23	100.0	24	11	US-09-833-245-7	Sequence 7, Appl
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249	23	357	12	US-10-282-122A-70593	Sequence 70593, A	322	23	100.0	484	12	US-10-406-686A-29	Sequence 29, Appl
250	23	357	12	US-10-282-122A-70674	Sequence 70674, A	323	23	100.0	484	12	US-10-335-977-6320	Sequence 6320, Ap
251	23	357	12	US-10-282-122A-70699	Sequence 70699, A	324	23	100.0	485	15	US-10-321-844-90	Sequence 90, Appl
252	23	357	12	US-10-282-122A-71069	Sequence 71069, A	325	23	100.0	485	15	US-10-369-493-16926	Sequence 16926, A
253	23	357	12	US-10-282-122A-71104	Sequence 71104, A	326	23	100.0	485	16	US-10-408-765A-2297	Sequence 2297, App
254	23	357	12	US-10-282-122A-71243	Sequence 71243, A	327	23	100.0	485	16	US-10-741-601-288	Sequence 288, App
255	23	360	9	US-09-815-242-11378	Sequence 11378, A	328	23	100.0	485	16	US-10-741-601-289	Sequence 289, App
256	23	360	12	US-10-282-122A-58823	Sequence 58823, A	329	23	100.0	496	9	US-09-312-762A-15	Sequence 15, Appl
257	23	360	12	US-10-425-114-42197	Sequence 42197, A	330	23	100.0	497	16	US-10-437-963-130126	Sequence 130126, A
258	23	360	12	US-10-335-977-6956	Sequence 6956, Ap	331	23	100.0	498	12	US-10-425-114-63735	Sequence 63735, A
259	23	363	12	US-10-424-599-143498	Sequence 143498, A	332	23	100.0	499	12	US-10-425-114-63937	Sequence 3397, A
260	23	368	12	US-10-425-114-70280	Sequence 70280, A	333	23	100.0	500	12	US-10-282-122A-54612	Sequence 54612, A
261	23	371	16	US-10-437-963-113971	Sequence 113971, A	334	23	100.0	501	15	US-10-453-763-4	Sequence 4, Appl
262	23	375	12	US-10-335-977-6957	Sequence 6957, Ap	335	23	100.0	503	15	US-10-369-493-4118	Sequence 4118, Ap
263	23	378	9	US-09-860-670-86	Sequence 86, Appl	336	23	100.0	504	15	US-10-369-493-12595	Sequence 12595, A
264	23	378	9	US-09-764-868-628	Sequence 628, App	337	23	100.0	505	14	US-10-156-761-11827	Sequence 11827, A
265	23	378	10	US-09-955-999-69	Sequence 69, Appl	338	23	100.0	508	14	US-10-465-217-1	Sequence 1, Appl
266	23	378	11	US-09-764-875-1153	Sequence 1153, Ap	339	23	100.0	508	14	US-10-434-588-4	Sequence 4, Appl
267	23	378	15	US-10-227-646-86	Sequence 86, Appl	340	23	100.0	510	12	US-10-282-122A-58366	Sequence 58366, A
268	23	380	16	US-10-437-963-191026	Sequence 191026, A	341	23	100.0	510	15	US-10-289-762-639	Sequence 639, App
269	23	382	12	US-10-424-599-246632	Sequence 246632, A	342	23	100.0	518	12	US-10-389-647-421	Sequence 421, App
270	23	388	15	US-10-369-493-21356	Sequence 21356, A	343	23	100.0	518	15	US-10-369-493-3533	Sequence 3533, Ap
271	23	389	15	US-10-369-493-23255	Sequence 23255, A	344	23	100.0	523	16	US-10-437-963-120061	Sequence 120061, A
272	23	389	16	US-10-437-963-148202	Sequence 148202, A	345	23	100.0	524	12	US-10-424-599-266029	Sequence 266029, A
273	23	394	12	US-10-627-476-224	Sequence 224, App	346	23	100.0	527	16	US-10-437-963-113042	Sequence 113042, A
274	23	396	15	US-10-369-493-8066	Sequence 8066, Ap	347	23	100.0	534	9	US-09-312-762A-5	Sequence 4, Appl
275	23	397	15	US-10-369-493-261	Sequence 261, App	348	23	100.0	534	9	US-09-312-762A-4	Sequence 5, Appl
276	23	400	15	US-10-369-493-21850	Sequence 21850, A	349	23	100.0	534	16	US-10-755-889-336	Sequence 336, App
277	23	402	15	US-10-369-493-3740	Sequence 3740, Ap	350	23	100.0	535	9	US-09-312-762A-10	Sequence 10, Appl
278	23	403	15	US-10-369-493-19185	Sequence 19185, A	351	23	100.0	535	9	US-09-312-762A-14	Sequence 14, Appl
279	23	412	11	US-09-930-512-75	Sequence 75, Appl	352	23	100.0	538	12	US-10-282-122A-49335	Sequence 49335, A
280	23	414	12	US-10-424-599-212448	Sequence 212448, A	353	23	100.0	538	16	US-10-408-765A-1137	Sequence 1137, Ap
281	23	417	15	US-10-369-493-10765	Sequence 10765, A	354	23	100.0	541	16	US-10-408-765A-2275	Sequence 2275, Ap
282	23	420	12	US-10-425-114-52818	Sequence 52818, A	355	23	100.0	543	16	US-10-408-765A-1720	Sequence 1720, Ap
283	23	420	15	US-10-369-493-10221	Sequence 10221, A	356	23	100.0	547	12	US-10-424-599-187086	Sequence 187086, A
284	23	422	15	US-10-289-762-1088	Sequence 1088, Ap	357	23	100.0	552	12	US-10-425-114-67035	Sequence 67035, A
285	23	423	15	US-10-023-634-83	Sequence 83, Appl	358	23	100.0	552	16	US-10-437-963-194394	Sequence 194394, A
286	23	432	15	US-10-369-493-9942	Sequence 9942, Ap	359	23	100.0	554	9	US-09-746-491-41	Sequence 41, Appl
287	23	435	15	US-10-369-493-10634	Sequence 10634, A	360	23	100.0	556	16	US-10-437-963-154446	Sequence 154446, A
288	23	436	15	US-10-369-493-2369	Sequence 2369, Ap	361	23	100.0	558	16	US-10-369-493-7749	Sequence 7749, Ap
289	23	436	15	US-10-369-493-18273	Sequence 18273, A	362	23	100.0	562	12	US-10-282-122A-50623	Sequence 50623, A
290	23	437	12	US-10-282-122A-51974	Sequence 51974, A	363	23	100.0	567	12	US-10-424-599-145717	Sequence 145717, A
291	23	440	15	US-10-369-493-23326	Sequence 23326, A	364	23	100.0	570	16	US-10-437-963-194392	Sequence 194392, A
292	23	441	15	US-10-369-493-17161	Sequence 17161, A	365	23	100.0	573	14	US-10-043-487-327	Sequence 327, App
293	23	444	16	US-10-287-226-370	Sequence 370, App	366	23	100.0	575	15	US-10-369-493-10343	Sequence 10343, A
294	23	444	16	US-10-287-226-372	Sequence 372, App	367	23	100.0	585	9	US-09-929-552-2	Sequence 2, Appl
295	23	445	12	US-10-282-122A-52444	Sequence 52444, A	368	23	100.0	585	10	US-09-932-613-445	Sequence 445, App
296	23	447	15	US-10-104-047-2123	Sequence 2123, Ap	369	23	100.0	585	10	US-09-984-010-26	Sequence 26, Appl
297	23	447	16	US-10-437-963-166961	Sequence 166961, A	370	23	100.0	585	10	US-09-833-041-18	Sequence 18, Appl
298	23	448	10	US-09-769-970-2	Sequence 2, Appl	371	23	100.0	585	10	US-09-833-117-18	Sequence 18, Appl
299	23	449	15	US-10-051-874-68	Sequence 68, Appl	372	23	100.0	585	10	US-09-932-322-445	Sequence 45, App
300	23	451	15	US-10-369-493-353	Sequence 353, App	373	23	100.0	585	10	US-09-832-501-18	Sequence 18, Appl
301	23	453	16	US-10-767-701-40181	Sequence 40181, A	374	23	100.0	585	11	US-09-833-115-18	Sequence 18, Appl
302	23	455	16	US-10-437-963-168134	Sequence 168134, A	375	23	100.0	585	11	US-09-833-245-18	Sequence 18, Appl
303	23	465	15	US-10-369-493-9941	Sequence 9941, Ap	376	23	100.0	585	12	US-10-424-999-11	Sequence 11, Appl
304	23	466	12	US-10-425-114-64356	Sequence 64356, A	377	23	100.0	585	12	US-10-425-000-31	Sequence 31, Appl
305	23	467	16	US-10-437-963-151306	Sequence 151306, A	378	23	100.0	585	12	US-10-425-000-34	Sequence 34, Appl
306	23	468	16	US-10-437-963-111279	Sequence 111279, A	379	23	100.0	585	12	US-10-602-141-39	Sequence 39, Appl
307	23	469	9	US-09-738-626-3908	Sequence 3908, Ap	380	23	100.0	585	12	US-09-832-929-18	Sequence 18, Appl



381	23	100.0	585	13	US-10-153-064-5	Sequence 5, Appl	454	23	100.0	660	14	US-10-153-604A-90	Sequence 90, Appl
382	23	100.0	585	14	US-10-153-604A-5	Sequence 5, Appl	455	23	100.0	660	14	US-10-153-604A-93	Sequence 93, Appl
383	23	100.0	585	14	US-10-319-263-1	Sequence 1, Appl	456	23	100.0	668	12	US-10-282-122A-72916	Sequence 72916, A
384	23	100.0	585	14	US-10-319-263-2	Sequence 2, Appl	457	23	100.0	668	12	US-10-153-064-102	Sequence 102, App
385	23	100.0	585	14	US-10-414-469-1	Sequence 1, Appl	458	23	100.0	668	14	US-10-153-604A-102	Sequence 102, App
386	23	100.0	585	14	US-10-414-469-2	Sequence 2, Appl	459	23	100.0	670	16	US-10-408-765A-996	Sequence 996, App
387	23	100.0	585	14	US-10-413-831-1	Sequence 1, Appl	460	23	100.0	671	16	US-10-363-829-452	Sequence 452, App
388	23	100.0	585	14	US-10-413-831-2	Sequence 2, Appl	461	23	100.0	672	12	US-10-424-999-15	Sequence 15, Appl
389	23	100.0	585	15	US-10-413-832-1	Sequence 1, Appl	462	23	100.0	672	12	US-10-425-000-35	Sequence 35, Appl
390	23	100.0	585	15	US-10-413-832-2	Sequence 2, Appl	463	23	100.0	672	15	US-10-233-675A-15	Sequence 15, Appl
391	23	100.0	585	15	US-10-414-386-1	Sequence 1, Appl	464	23	100.0	674	12	US-10-424-999-14	Sequence 14, Appl
392	23	100.0	585	15	US-10-414-386-2	Sequence 2, Appl	465	23	100.0	674	12	US-10-425-000-34	Sequence 34, Appl
393	23	100.0	585	15	US-10-233-675A-11	Sequence 11, Appl	466	23	100.0	674	15	US-10-233-675A-14	Sequence 14, Appl
394	23	100.0	585	15	US-10-462-362-26	Sequence 26, Appl	467	23	100.0	674	16	US-10-437-963-160252	Sequence 160252
395	23	100.0	585	16	US-10-361-997-18	Sequence 18, Appl	468	23	100.0	676	13	US-10-153-064-95	Sequence 95, Appl
396	23	100.0	592	12	US-10-042-865-64	Sequence 64, Appl	469	23	100.0	676	13	US-10-153-064-98	Sequence 98, Appl
397	23	100.0	597	14	US-10-017-161-800	Sequence 800, App	470	23	100.0	676	13	US-10-153-064-104	Sequence 104, App
398	23	100.0	604	10	US-09-984-010-7	Sequence 7, Appl	471	23	100.0	676	13	US-10-153-064-127	Sequence 127, App
399	23	100.0	604	16	US-10-408-765A-55	Sequence 55, Appl	472	23	100.0	676	13	US-10-153-064-129	Sequence 129, App
400	23	100.0	609	10	US-09-919-039-370	Sequence 370, App	473	23	100.0	676	14	US-10-153-064A-95	Sequence 95, Appl
401	23	100.0	609	12	US-10-424-999-215539	Sequence 215539, App	474	23	100.0	676	14	US-10-153-064A-98	Sequence 98, Appl
402	23	100.0	609	12	US-10-609-346-12	Sequence 12, Appl	475	23	100.0	676	14	US-10-153-604A-104	Sequence 104, App
403	23	100.0	609	13	US-10-153-064-7	Sequence 7, Appl	476	23	100.0	676	14	US-10-153-604A-127	Sequence 127, App
404	23	100.0	609	14	US-10-153-604A-7	Sequence 7, Appl	477	23	100.0	676	14	US-10-153-604A-129	Sequence 129, App
405	23	100.0	609	14	US-10-365-623-23	Sequence 23, Appl	478	23	100.0	677	13	US-10-153-064-125	Sequence 125, App
406	23	100.0	609	16	US-10-408-765A-2	Sequence 2, Appl	479	23	100.0	677	14	US-10-153-604A-125	Sequence 125, App
407	23	100.0	610	9	US-09-984-186-2	Sequence 2, Appl	480	23	100.0	678	16	US-10-437-963-105320	Sequence 105320, App
408	23	100.0	610	14	US-10-237-667-2	Sequence 2, Appl	481	23	100.0	680	13	US-10-153-064-123	Sequence 123, App
409	23	100.0	610	14	US-10-237-708-2	Sequence 2, Appl	482	23	100.0	680	14	US-10-153-604A-123	Sequence 123, App
410	23	100.0	610	14	US-10-237-866-2	Sequence 2, Appl	483	23	100.0	680	14	US-10-153-064-92	Sequence 92, Appl
411	23	100.0	610	14	US-10-237-871-2	Sequence 2, Appl	484	23	100.0	680	14	US-10-153-604A-92	Sequence 92, Appl
412	23	100.0	610	14	US-10-237-624-2	Sequence 2, Appl	485	23	100.0	687	12	US-10-424-999-17	Sequence 17, Appl
413	23	100.0	610	16	US-10-702-536-2	Sequence 2, Appl	486	23	100.0	687	12	US-10-425-000-37	Sequence 37, Appl
414	23	100.0	610	16	US-10-702-536-2	Sequence 2, Appl	487	23	100.0	687	12	US-10-233-675A-17	Sequence 17, Appl
415	23	100.0	610	16	US-10-767-701-46127	Sequence 46127, A	488	23	100.0	688	12	US-10-424-999-18	Sequence 18, Appl
416	23	100.0	615	12	US-10-282-122A-47612	Sequence 47612, A	489	23	100.0	688	12	US-10-425-000-38	Sequence 38, Appl
417	23	100.0	615	12	US-10-282-122A-49108	Sequence 49108, A	490	23	100.0	688	15	US-10-233-675A-18	Sequence 18, Appl
418	23	100.0	616	12	US-10-433-108-13	Sequence 13, Appl	491	23	100.0	689	12	US-10-424-999-13	Sequence 13, Appl
419	23	100.0	617	16	US-10-361-997-64	Sequence 64, Appl	492	23	100.0	689	12	US-10-425-000-33	Sequence 33, Appl
420	23	100.0	617	16	US-10-361-997-77	Sequence 77, Appl	493	23	100.0	689	15	US-10-233-675A-13	Sequence 13, Appl
421	23	100.0	624	12	US-10-433-108-16	Sequence 16, Appl	494	23	100.0	692	13	US-10-153-064-101	Sequence 101, App
422	23	100.0	624	12	US-10-433-108-16	Sequence 16, Appl	495	23	100.0	692	14	US-10-153-604A-101	Sequence 101, App
423	23	100.0	626	12	US-10-424-999-249044	Sequence 249044, A	496	23	100.0	694	16	US-10-361-997-71	Sequence 71, Appl
424	23	100.0	629	14	US-10-156-761-14676	Sequence 14676, A	497	23	100.0	694	16	US-10-424-999-283233	Sequence 283233, App
425	23	100.0	631	12	US-10-433-108-14	Sequence 14, Appl	498	23	100.0	701	12	US-10-424-999-283233	Sequence 283233, App
426	23	100.0	631	15	US-10-369-493-4973	Sequence 4973, Ap	499	23	100.0	702	9	US-03-815-242-10117	Sequence 10117, A
427	23	100.0	632	16	US-10-437-963-126138	Sequence 126138, A	500	23	100.0	705	12	US-09-848-909-25	Sequence 25, Appl
428	23	100.0	638	16	US-10-361-997-69	Sequence 69, Appl	501	23	100.0	710	15	US-10-054-435-2	Sequence 2, Appl
429	23	100.0	639	12	US-10-282-122A-48592	Sequence 48592, A	502	23	100.0	711	12	US-10-282-122A-67509	Sequence 67509, A
430	23	100.0	640	12	US-10-433-108-15	Sequence 15, Appl	503	23	100.0	712	12	US-09-848-909-27	Sequence 27, Appl
431	23	100.0	640	12	US-10-433-108-17	Sequence 17, Appl	504	23	100.0	712	12	US-10-609-346-10	Sequence 10, Appl
432	23	100.0	651	13	US-10-153-064-133	Sequence 133, App	505	23	100.0	714	9	US-03-828-303-21	Sequence 21, Appl
433	23	100.0	651	14	US-10-153-604A-133	Sequence 133, App	506	23	100.0	714	16	US-10-716-089-21	Sequence 21, Appl
434	23	100.0	652	13	US-10-153-064-96	Sequence 96, Appl	507	23	100.0	717	15	US-10-369-493-2178	Sequence 2178, Ap
435	23	100.0	652	13	US-10-153-064-99	Sequence 99, Appl	508	23	100.0	718	12	US-10-609-346-4	Sequence 4, Appl
436	23	100.0	652	13	US-10-153-064-105	Sequence 105, App	509	23	100.0	723	14	US-10-083-357-1343	Sequence 1343, Ap
437	23	100.0	652	13	US-10-153-064-132	Sequence 132, App	510	23	100.0	723	14	US-10-437-963-203858	Sequence 203858, A
438	23	100.0	652	14	US-10-153-064A-96	Sequence 96, Appl	511	23	100.0	727	16	US-10-369-493-23085	Sequence 23085, A
439	23	100.0	652	14	US-10-153-064A-99	Sequence 99, Appl	512	23	100.0	728	16	US-10-361-997-75	Sequence 75, Appl
440	23	100.0	652	14	US-10-153-604A-105	Sequence 105, App	513	23	100.0	729	16	US-10-361-997-46	Sequence 46, Appl
441	23	100.0	652	14	US-10-153-604A-132	Sequence 132, App	514	23	100.0	731	15	US-10-108-260A-2451	Sequence 2451, Ap
442	23	100.0	653	13	US-10-153-064-131	Sequence 131, App	515	23	100.0	734	14	US-10-128-714-3042	Sequence 3042, Ap
443	23	100.0	653	14	US-10-153-604A-131	Sequence 131, App	516	23	100.0	738	14	US-10-270-333-6	Sequence 6, Appl
444	23	100.0	653	16	US-10-437-963-130122	Sequence 130122, A	517	23	100.0	742	12	US-10-424-999-227627	Sequence 227627, App
445	23	100.0	655	16	US-10-361-997-59	Sequence 59, Appl	518	23	100.0	743	16	US-10-149-310-208	Sequence 208, App
446	23	100.0	655	16	US-10-361-997-61	Sequence 61, Appl	519	23	100.0	746	12	US-10-609-346-6	Sequence 6, Appl
447	23	100.0	656	14	US-10-153-064-130	Sequence 130, App	520	23	100.0	749	16	US-10-282-122A-55747	Sequence 55747, A
448	23	100.0	656	14	US-10-153-604A-130	Sequence 130, App	521	23	100.0	749	16	US-10-437-963-200587	Sequence 200587, A
449	23	100.0	659	16	US-10-361-997-52	Sequence 52, Appl	522	23	100.0	750	9	US-09-815-242-13985	Sequence 13985, A
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451	23	100.0	659	16	US-10-361-997-57	Sequence 57, Appl	524	23	100.0	752	16	US-10-361-997-74	Sequence 74, Appl
452	23	100.0	660	13	US-10-153-064-90	Sequence 90, Appl	525	23	100.0	753	9	US-09-815-242-10181	Sequence 10181, A
453	23	100.0	660	13	US-10-153-064-93	Sequence 93, Appl	526	23	100.0	753	12	US-10-282-122A-42878	Sequence 42878, A

527	23	100.0	753	12	US-10-424-599-187090	Sequence 187090,	600	23	100.0	1583	16	US-10-408-765A-1635	Sequence 1635, Ap
528	23	100.0	753	15	US-10-369-493-854	Sequence 854, App	601	23	100.0	1604	9	US-09-746-491-8	Sequence 8, Appli
529	23	100.0	753	16	US-10-361-997-45	Sequence 45, Appl	602	23	100.0	1855	16	US-10-437-963-144021	Sequence 144021
530	23	100.0	754	12	US-10-424-599-187084	Sequence 187084,	603	23	100.0	1917	16	US-10-408-765A-1313	Sequence 1313, Ap
531	23	100.0	759	12	US-10-609-346-8	Sequence 8, Appli	604	23	100.0	1967	10	US-09-849-603-16	Sequence 11, Appl
532	23	100.0	763	12	US-10-609-346-2	Sequence 2, Appli	605	23	100.0	2051	16	US-10-473-575-11	Sequence 11, Appl
533	23	100.0	787	9	US-09-984-186-16	Sequence 16, Appl	606	23	100.0	2107	12	US-10-087-192-2025	Sequence 2025, Ap
534	23	100.0	787	14	US-10-237-667-16	Sequence 16, Appl	607	23	100.0	2215	14	US-10-281-478-4	Sequence 4, Appli
535	23	100.0	787	14	US-10-237-708-16	Sequence 16, Appl	608	23	100.0	2280	16	US-10-437-963-201203	Sequence 201203,
536	23	100.0	787	14	US-10-237-866-16	Sequence 16, Appl	609	23	100.0	2457	12	US-10-282-122A-49854	Sequence 49854, A
537	23	100.0	787	14	US-10-237-871-16	Sequence 16, Appl	610	23	100.0	2671	16	US-10-408-765A-442	Sequence 442, App
538	23	100.0	787	14	US-10-237-624-16	Sequence 16, Appl	611	23	100.0	3079	15	US-10-369-493-2024	Sequence 2024, Ap
539	23	100.0	787	15	US-10-108-260A-3773	Sequence 3773, Ap	612	23	100.0	3084	9	US-09-938-275-4	Sequence 4, Appli
540	23	100.0	787	16	US-10-702-536-16	Sequence 16, Appl	613	23	100.0	3084	14	US-10-262-670-2	Sequence 2, Appli
541	23	100.0	787	16	US-10-702-636-16	Sequence 16, Appl	614	23	100.0	3542	12	US-10-087-013-2	Sequence 2, Appli
542	23	100.0	788	9	US-09-908-193-35	Sequence 35, Appl	615	23	100.0	3632	12	US-10-282-122A-71235	Sequence 71235, A
543	23	100.0	788	14	US-10-073-118-26	Sequence 26, Appl	616	23	100.0	4861	9	US-09-919-497-70	Sequence 70, Appl
544	23	100.0	789	16	US-10-437-963-183376	Sequence 183376,	617	23	100.0	4861	14	US-10-097-534-26	Sequence 26, Appl
545	23	100.0	791	15	US-10-320-800-16	Sequence 16, Appl	618	23	100.0	4861	14	US-10-146-473-49	Sequence 49, Appl
546	23	100.0	796	14	US-10-276-629-16	Sequence 16, Appl	619	23	100.0	4952	15	US-10-051-874-56	Sequence 56, Appl
547	23	100.0	803	16	US-10-389-566-1942	Sequence 16, Appl	620	23	100.0	5008	15	US-10-051-874-166	Sequence 166, App
548	23	100.0	808	15	US-10-369-493-6771	Sequence 1942, Ap	621	23	100.0	5159	15	US-10-085-198-112	Sequence 112, App
549	23	100.0	810	9	US-09-712-363-281	Sequence 6771, Ap	622	23	100.0	5262	15	US-10-051-874-165	Sequence 165, App
550	23	100.0	814	15	US-10-369-493-1953	Sequence 1953, Ap	623	23	100.0	5262	15	US-10-051-874-167	Sequence 167, App
551	23	100.0	824	16	US-10-408-765A-1997	Sequence 1997, Ap	624	23	100.0	5262	16	US-10-408-765A-741	Sequence 741, App
552	23	100.0	834	16	US-10-437-963-115995	Sequence 115995,	625	20	87.0	4	14	US-10-205-110-37	Sequence 37, Appl
553	23	100.0	834	16	US-10-437-963-115995	Sequence 53919, A	626	20	87.0	7	12	US-09-764-918-5	Sequence 5, Appli
554	23	100.0	865	12	US-10-282-122A-42896	Sequence 42896, A	627	20	87.0	7	12	US-09-768-183-5	Sequence 5, Appli
555	23	100.0	871	12	US-10-282-122A-54240	Sequence 54240, A	628	20	87.0	8	10	US-09-827-542-13	Sequence 13, Appl
556	23	100.0	876	12	US-10-282-122A-77326	Sequence 77326, A	629	20	87.0	9	14	US-10-286-457-301	Sequence 301, App
557	23	100.0	876	12	US-09-848-909-31	Sequence 31, Appl	630	20	87.0	13	12	US-09-764-918-8	Sequence 8, Appli
558	23	100.0	879	12	US-10-472-146-2	Sequence 31, Appl	631	20	87.0	13	12	US-09-768-183-8	Sequence 8, Appli
559	23	100.0	883	16	US-10-472-146-2	Sequence 2, Appli	632	20	87.0	13	15	US-10-436-715-418	Sequence 418, App
560	23	100.0	883	16	US-10-472-146-4	Sequence 4, Appli	633	20	87.0	15	10	US-09-977-797A-136	Sequence 136, App
561	23	100.0	883	16	US-10-472-146-6	Sequence 6, Appli	634	20	87.0	18	14	US-10-174-410-30	Sequence 30, Appl
562	23	100.0	883	16	US-10-472-146-8	Sequence 8, Appli	635	20	87.0	20	14	US-10-174-410-65	Sequence 65, Appl
563	23	100.0	883	16	US-10-472-146-10	Sequence 10, Appl	636	20	87.0	21	14	US-10-029-386-28018	Sequence 28018, A
564	23	100.0	883	16	US-10-472-146-12	Sequence 12, Appl	637	20	87.0	22	14	US-10-247-279-11	Sequence 11, Appl
565	23	100.0	883	16	US-10-472-146-14	Sequence 14, Appl	638	20	87.0	25	9	US-09-864-761-45705	Sequence 45705, A
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568	23	100.0	919	15	US-10-369-493-6768	Sequence 6768, Ap	641	20	87.0	34	12	US-10-424-599-169789	Sequence 169789,
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572	23	100.0	949	12	US-10-211-462-30	Sequence 30, Appl	645	20	87.0	39	9	US-09-864-761-46328	Sequence 46328, A
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577	23	100.0	966	16	US-10-437-963-134857	Sequence 134857,	650	20	87.0	47	12	US-10-424-599-218462	Sequence 218462,
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582	23	100.0	1043	12	US-10-282-122A-50102	Sequence 50102, A	655	20	87.0	48	12	US-10-004-860-511	Sequence 511, App
583	23	100.0	1087	12	US-10-424-599-189678	Sequence 189678,	656	20	87.0	48	14	US-10-023-282-511	Sequence 511, App
584	23	100.0	1098	15	US-10-161-927-18	Sequence 18, Appl	657	20	87.0	51	9	US-09-867-550-874	Sequence 874, App
585	23	100.0	1129	15	US-10-369-493-11078	Sequence 11078, A	658	20	87.0	51	12	US-10-424-599-227267	Sequence 227267,
586	23	100.0	1158	15	US-10-369-493-6899	Sequence 6899, Ap	659	20	87.0	52	12	US-10-424-599-201286	Sequence 201286,
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593	23	100.0	1247	15	US-10-161-493-70	Sequence 70, Appl	666	20	87.0	56	12	US-10-424-599-220552	Sequence 220552,
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595	23	100.0	1314	14	US-10-156-761-13242	Sequence 13242, A	668	20	87.0	58	11	US-09-864-408A-3988	Sequence 3988, Ap
596	23	100.0	1421	16	US-10-437-963-149400	Sequence 149400,	669	20	87.0	58	12	US-10-424-599-225277	Sequence 225277,
597	23	100.0	1465	14	US-10-083-357-1310	Sequence 1310, Ap	670	20	87.0	58	16	US-10-437-963-178197	Sequence 178197,
598	23	100.0	1572	16	US-10-437-963-116757	Sequence 116757,	671	20	87.0	59	12	US-10-424-599-173804	Sequence 173804,
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703	20	87.0	83	12	US-10-424-599-252858	Sequence 252858,	776	120	9	US-09-989-279-399	Sequence 399, App
704	20	87.0	83	16	US-10-437-963-107781	Sequence 107781,	777	120	9	US-09-989-727-399	Sequence 399, App
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706	20	87.0	84	12	US-10-424-599-236181	Sequence 236181,	779	120	9	US-09-989-732-399	Sequence 399, App
707	20	87.0	84	12	US-10-424-599-255371	Sequence 255371,	780	120	9	US-09-991-073-399	Sequence 399, App
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715	20	87.0	87	11	US-09-833-245-445	Sequence 445, App	788	120	9	US-09-989-735-399	Sequence 399, App
716	20	87.0	87	12	US-10-424-599-191914	Sequence 191914,	789	120	9	US-09-990-444-399	Sequence 399, App
717	20	87.0	87	16	US-10-437-963-198861	Sequence 198861,	790	120	9	US-09-991-181-399	Sequence 399, App
718	20	87.0	88	10	US-09-933-767-730	Sequence 730, App	791	120	9	US-09-989-730-399	Sequence 399, App
719	20	87.0	88	12	US-10-424-599-156562	Sequence 156562,	792	120	9	US-09-990-436-399	Sequence 399, App
720	20	87.0	88	12	US-10-004-860-730	Sequence 163941,	793	120	9	US-09-993-687-399	Sequence 399, App
721	20	87.0	88	12	US-10-023-282-730	Sequence 730, App	794	120	10	US-09-989-734-399	Sequence 399, App
722	20	87.0	88	14	US-10-134-841-1	Sequence 1, Appli	795	120	10	US-09-997-653-399	Sequence 399, App
723	20	87.0	89	14	US-10-316-253-46	Sequence 46, Appl	796	120	10	US-09-993-667-399	Sequence 399, App
724	20	87.0	89	16	US-10-624-631-32	Sequence 32, Appl	797	120	10	US-09-997-428-399	Sequence 399, App
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730	20	87.0	91	12	US-10-424-599-216403	Sequence 216403,	803	120	10	US-09-998-156-399	Sequence 399, App
731	20	87.0	91	12	US-10-424-599-237394	Sequence 237394,	804	120	10	US-09-990-437-399	Sequence 399, App
732	20	87.0	92	12	US-10-437-963-196809	Sequence 196809,	805	120	10	US-09-991-157-399	Sequence 399, App
733	20	87.0	96	16	US-10-437-963-148781	Sequence 148781, A	806	120	10	US-09-997-514-399	Sequence 399, App
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735	20	87.0	97	16	US-10-767-701-31653	Sequence 31653, A	808	120	10	US-09-991-172-399	Sequence 399, App
736	20	87.0	98	16	US-10-299-636-39	Sequence 39, Appl	809	120	10	US-09-990-726-399	Sequence 399, App
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738	20	87.0	99	11	US-09-864-408A-5032	Sequence 5032, Ap	811	120	10	US-09-997-601-399	Sequence 399, App
739	20	87.0	99	16	US-10-437-963-110025	Sequence 110025,	812	120	10	US-09-990-443-399	Sequence 399, App
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741	20	87.0	101	16	US-10-437-963-144473	Sequence 144473,	814	120	10	US-09-997-628-399	Sequence 399, App
742	20	87.0	101	16	US-10-437-963-137869	Sequence 137869,	815	120	10	US-09-997-683-399	Sequence 399, App
743	20	87.0	103	16	US-10-437-963-187536	Sequence 187536,	816	120	10	US-09-989-729A-399	Sequence 399, App
744	20	87.0	103	16	US-09-867-550-280	Sequence 280, App	817	120	10	US-09-997-349-399	Sequence 399, App
745	20	87.0	104	9			818	120	10	US-09-997-440-399	Sequence 399, App

819	20	87.0	120	10	US-09-990-440-399	Sequence 399, App	892	20	87.0	120	14	US-10-216-164-98	Sequence 98, Appl
820	20	87.0	120	10	US-09-993-469-399	Sequence 399, App	893	20	87.0	120	14	US-10-216-167-98	Sequence 98, Appl
821	20	87.0	120	10	US-09-997-542-399	Sequence 399, App	894	20	87.0	120	14	US-10-216-168-98	Sequence 98, Appl
822	20	87.0	120	10	US-09-993-748-399	Sequence 399, App	895	20	87.0	120	14	US-10-219-065-98	Sequence 98, Appl
823	20	87.0	120	10	US-09-990-439-399	Sequence 399, App	896	20	87.0	120	14	US-10-219-071-98	Sequence 98, Appl
824	20	87.0	120	10	US-09-990-427-399	Sequence 399, App	897	20	87.0	120	14	US-10-219-074-98	Sequence 98, Appl
825	20	87.0	120	10	US-09-989-328-399	Sequence 399, App	898	20	87.0	120	14	US-10-219-077-98	Sequence 98, Appl
826	20	87.0	120	10	US-09-993-583-399	Sequence 399, App	899	20	87.0	120	14	US-10-219-465-98	Sequence 98, Appl
827	20	87.0	120	10	US-09-941-992-399	Sequence 399, App	900	20	87.0	120	14	US-10-219-467-98	Sequence 98, Appl
828	20	87.0	120	10	US-09-992-521-399	Sequence 399, App	901	20	87.0	120	14	US-10-219-469-98	Sequence 98, Appl
829	20	87.0	120	10	US-09-997-333-399	Sequence 399, App	902	20	87.0	120	14	US-10-219-471-98	Sequence 98, Appl
830	20	87.0	120	10	US-09-997-384-399	Sequence 399, App	903	20	87.0	120	14	US-10-219-473-98	Sequence 98, Appl
831	20	87.0	120	10	US-09-998-041-399	Sequence 399, App	904	20	87.0	120	14	US-10-219-476-98	Sequence 98, Appl
832	20	87.0	120	10	US-09-997-585-399	Sequence 399, App	905	20	87.0	120	14	US-10-219-482-98	Sequence 98, Appl
833	20	87.0	120	10	US-09-997-614-399	Sequence 399, App	906	20	87.0	120	14	US-10-227-874-98	Sequence 98, Appl
834	20	87.0	120	10	US-09-989-862-399	Sequence 399, App	907	20	87.0	120	14	US-10-227-876-98	Sequence 98, Appl
835	20	87.0	120	10	US-09-997-529-399	Sequence 399, App	908	20	87.0	120	14	US-10-227-878-98	Sequence 98, Appl
836	20	87.0	120	10	US-09-989-725-399	Sequence 399, App	909	20	87.0	120	14	US-10-229-974-98	Sequence 98, Appl
837	20	87.0	120	10	US-09-989-733-399	Sequence 399, App	910	20	87.0	120	14	US-10-230-024-98	Sequence 98, Appl
838	20	87.0	120	11	US-09-992-643-399	Sequence 399, App	911	20	87.0	120	14	US-10-230-113-98	Sequence 98, Appl
839	20	87.0	120	12	US-10-424-593-168100	Sequence 168100, App	912	20	87.0	120	14	US-10-230-183-98	Sequence 98, Appl
840	20	87.0	120	12	US-10-219-535-98	Sequence 98, Appl	913	20	87.0	120	14	US-10-230-234-98	Sequence 98, Appl
841	20	87.0	120	12	US-10-232-230-98	Sequence 98, Appl	914	20	87.0	120	14	US-10-230-306-98	Sequence 98, Appl
842	20	87.0	120	12	US-09-989-724-399	Sequence 399, App	915	20	87.0	120	14	US-10-230-426-98	Sequence 98, Appl
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844	20	87.0	120	12	US-09-990-441-399	Sequence 399, App	917	20	87.0	120	14	US-10-230-433-98	Sequence 98, Appl
845	20	87.0	120	12	US-09-997-857-399	Sequence 399, App	918	20	87.0	120	14	US-10-230-438-98	Sequence 98, Appl
846	20	87.0	120	12	US-10-232-224-98	Sequence 98, Appl	919	20	87.0	120	14	US-10-232-222-98	Sequence 98, Appl
847	20	87.0	120	12	US-09-997-641-399	Sequence 399, App	920	20	87.0	120	14	US-10-219-070-98	Sequence 98, Appl
848	20	87.0	120	12	US-09-991-150-399	Sequence 399, App	921	20	87.0	120	14	US-10-219-472-98	Sequence 98, Appl
849	20	87.0	120	14	US-10-227-884-98	Sequence 98, Appl	922	20	87.0	120	14	US-10-219-527-98	Sequence 98, Appl
850	20	87.0	120	14	US-10-230-163-98	Sequence 98, Appl	923	20	87.0	120	14	US-10-227-877-98	Sequence 98, Appl
851	20	87.0	120	14	US-10-230-338-98	Sequence 98, Appl	924	20	87.0	120	14	US-10-216-166-98	Sequence 98, Appl
852	20	87.0	120	14	US-10-218-631-98	Sequence 98, Appl	925	20	87.0	120	14	US-10-218-612-98	Sequence 98, Appl
853	20	87.0	120	14	US-10-230-414-98	Sequence 98, Appl	926	20	87.0	120	14	US-10-218-163-98	Sequence 98, Appl
854	20	87.0	120	14	US-10-216-159A-98	Sequence 98, Appl	927	20	87.0	120	14	US-10-218-765-98	Sequence 98, Appl
855	20	87.0	120	14	US-10-218-849-98	Sequence 98, Appl	928	20	87.0	120	14	US-10-219-063-98	Sequence 98, Appl
856	20	87.0	120	14	US-10-227-873-98	Sequence 98, Appl	929	20	87.0	120	14	US-10-219-066-98	Sequence 98, Appl
857	20	87.0	120	14	US-10-227-876-98	Sequence 98, Appl	930	20	87.0	120	14	US-10-219-067-98	Sequence 98, Appl
858	20	87.0	120	14	US-10-219-073-98	Sequence 98, Appl	931	20	87.0	120	14	US-10-219-068-98	Sequence 98, Appl
859	20	87.0	120	14	US-10-230-434-98	Sequence 98, Appl	932	20	87.0	120	14	US-10-219-069-98	Sequence 98, Appl
860	20	87.0	120	14	US-10-219-003-98	Sequence 98, Appl	933	20	87.0	120	14	US-10-219-073-98	Sequence 98, Appl
861	20	87.0	120	14	US-10-219-075-98	Sequence 98, Appl	934	20	87.0	120	14	US-10-219-475-98	Sequence 98, Appl
862	20	87.0	120	14	US-10-219-464-98	Sequence 98, Appl	935	20	87.0	120	14	US-10-219-480-98	Sequence 98, Appl
863	20	87.0	120	14	US-10-219-466-98	Sequence 98, Appl	936	20	87.0	120	14	US-10-219-483-98	Sequence 98, Appl
864	20	87.0	120	14	US-10-219-479-98	Sequence 98, Appl	937	20	87.0	120	14	US-10-219-525-98	Sequence 98, Appl
865	20	87.0	120	14	US-10-219-481-98	Sequence 98, Appl	938	20	87.0	120	14	US-10-219-526-98	Sequence 98, Appl
866	20	87.0	120	14	US-10-230-260-98	Sequence 98, Appl	939	20	87.0	120	14	US-10-219-530-98	Sequence 98, Appl
867	20	87.0	120	14	US-10-232-231-98	Sequence 98, Appl	940	20	87.0	120	14	US-10-232-228-98	Sequence 98, Appl
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869	20	87.0	120	14	US-10-216-165-98	Sequence 98, Appl	942	20	87.0	120	14	US-10-219-533-98	Sequence 98, Appl
870	20	87.0	120	14	US-10-218-556-98	Sequence 98, Appl	943	20	87.0	120	14	US-10-219-538-399	Sequence 399, App
871	20	87.0	120	14	US-10-219-468-98	Sequence 98, Appl	944	20	87.0	120	14	US-10-232-229-98	Sequence 98, Appl
872	20	87.0	120	14	US-10-219-478-98	Sequence 98, Appl	945	20	87.0	120	14	US-10-232-228-98	Sequence 98, Appl
873	20	87.0	120	14	US-10-219-536-98	Sequence 98, Appl	946	20	87.0	120	15	US-10-219-538-399	Sequence 399, App
874	20	87.0	120	14	US-10-233-205-98	Sequence 98, Appl	947	20	87.0	120	15	US-10-232-226-98	Sequence 98, Appl
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877	20	87.0	120	14	US-10-219-474-98	Sequence 98, Appl	950	20	87.0	121	15	US-10-108-260A-2552	Sequence 2552, App
878	20	87.0	120	14	US-10-219-524-98	Sequence 98, Appl	951	20	87.0	121	16	US-10-437-963-153195	Sequence 153195, App
879	20	87.0	120	14	US-10-219-528-98	Sequence 98, Appl	952	20	87.0	122	16	US-10-424-599-277486	Sequence 277486, App
880	20	87.0	120	14	US-10-227-880-98	Sequence 98, Appl	953	20	87.0	122	16	US-10-437-963-123874	Sequence 123874, App
881	20	87.0	120	14	US-10-227-881-98	Sequence 98, Appl	954	20	87.0	123	10	US-09-954-9878-12	Sequence 123874, App
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883	20	87.0	120	14	US-10-230-436-98	Sequence 98, Appl	956	20	87.0	125	11	US-09-864-408A-3376	Sequence 3376, App
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887	20	87.0	120	14	US-10-232-229-98	Sequence 98, Appl	960	20	87.0	127	12	US-10-425-114-43360	Sequence 43360, A
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889	20	87.0	120	14	US-10-219-060-98	Sequence 98, Appl	962	20	87.0	130	11	US-09-864-408A-2866	Sequence 2866, App
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965 20 87.0 132 16 US-10-437-963-119433  
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998 20 87.0 146 12 US-10-424-599-152951  
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## ALIGNMENTS

RESULT 1  
US-10-199-285-1  
; Sequence 1, Application US/10199285  
; Publication No. US20030055003A1  
; GENERAL INFORMATION:  
; APPLICANT: DMI Biosciences, Inc.  
; APPLICANT: Yuki, Richard L.  
; TITLE OF INVENTION: USE OF COPPER CHELATORS TO INHIBIT THE INACTIVATION OF PROTEIN C  
; FILE REFERENCE: 4172-69  
; CURRENT APPLICATION NUMBER: US/10/199,285  
; PRIOR FILING DATE: 2002-07-19  
; PRIOR APPLICATION NUMBER: 60/307,005  
; PRIOR FILING DATE: 2001-07-19  
; PRIOR APPLICATION NUMBER: 60/344,514  
; PRIOR FILING DATE: 2001-12-28  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-199-285-1

Query Match 100.0%; Score 23; DB 14; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAHK 4  
Db 1 DAHK 4

RESULT 2  
US-10-076-071-1  
; Sequence 1, Application US/10076071  
; Publication No. US20030060408A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Or, David  
; APPLICANT: Curtis, C. Gerald  
; APPLICANT: Lau, Edward  
; APPLICANT: Rao, Nagaraja K.R.  
; APPLICANT: Winkler, James V.  
; TITLE OF INVENTION: Metal-Binding Compounds and Uses Therefor  
; FILE REFERENCE: 4172-3-2  
; CURRENT APPLICATION NUMBER: US/10/076,071  
; CURRENT FILING DATE: 2002-02-13  
; PRIOR APPLICATION NUMBER: 09/678,202  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/283,507  
; PRIOR FILING DATE: 2001-04-11  
; PRIOR APPLICATION NUMBER: 09/816,679  
; PRIOR FILING DATE: 2001-03-22  
; PRIOR APPLICATION NUMBER: 60/157,404  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,404  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/211,078  
; PRIOR FILING DATE: 2000-06-13  
; PRIOR APPLICATION NUMBER: 60/268,558  
; PRIOR FILING DATE: 2001-02-13  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-076-071-1

Query Match 100.0%; Score 23; DB 14; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 DAHK 4  
Db 1 DAHK 4

RESULT 3  
US-10-186-168-1  
; Sequence 1, Application US/10186168  
; Publication No. US20030130185A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Or, David  
; APPLICANT: Curtis, C. G.  
; APPLICANT: Lau, Edward  
; APPLICANT: Rao, Nagaraja K.R.  
; APPLICANT: Winkler, James V.  
; APPLICANT: Crook, Wannell M.  
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR  
; FILE REFERENCE: 4172-3  
; CURRENT APPLICATION NUMBER: US/10/186,168  
; CURRENT FILING DATE: 2002-06-27  
; PRIOR APPLICATION NUMBER: US/09/678,202  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/157,404  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/211,078  
; PRIOR FILING DATE: 2000-06-13  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT

; ORGANISM: Homo sapiens  
US-10-186-168-1

Query Match 100.0%; Score 23; DB 14; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
Db 1 DAHK 4

## RESULT 4

US-10-205-110-35  
; Sequence 35, Application US/10205110  
; Publication No. US20030144471A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonassen, Ib  
; APPLICANT: Egel-Mitani, Michi  
; APPLICANT: Balschmidt, Per  
; APPLICANT: Markussen, Jan  
; APPLICANT: Diers, Ivan  
; APPLICANT: Kjeldsen, Thomas Borglum  
; TITLE OF INVENTION: Method for Making Acylated Polypeptides  
; FILE REFERENCE: 6289,200-US  
; CURRENT APPLICATION NUMBER: US/10/205,110  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: PA 2001 01141  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/310,793  
; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-205-110-35

Query Match 100.0%; Score 23; DB 14; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
Db 1 DAHK 4

## RESULT 5

US-10-300-664-1  
; Sequence 1, Application US/10300664  
; Publication No. US20030158111A1  
; GENERAL INFORMATION:  
; APPLICANT: Bar-Or, David  
; APPLICANT: Curtis, C. G.  
; APPLICANT: Lau, Edward  
; APPLICANT: Rao, Nagarajo K.R.  
; APPLICANT: Winkler, James V.  
; APPLICANT: Crook, Wanneil M.  
; TITLE OF INVENTION: METAL BINDING COMPOUNDS AND USES THEREFOR  
; FILE REFERENCE: 4172-3  
; CURRENT APPLICATION NUMBER: US/10/300,664  
; CURRENT FILING DATE: 2002-11-19  
; PRIOR APPLICATION NUMBER: US/09/678,202  
; PRIOR FILING DATE: 2000-09-29  
; PRIOR APPLICATION NUMBER: 60/157,404  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/211,078  
; PRIOR FILING DATE: 2000-06-13  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-300-664-1

Query Match 100.0%; Score 23; DB 14; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
Db 1 DAHK 4

## RESULT 6

US-10-436-549-374  
; Sequence 374, Application US/10436549  
; Publication No. US20040038307A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank D.  
; APPLICANT: Meng, Dr. Xun  
; APPLICANT: Chan, John W.  
; APPLICANT: Zhang, Shengsheng  
; APPLICANT: Benkovic, Stephen J.  
; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN  
; TITLE OF INVENTION: PROTEIN ANALYSIS  
; FILE REFERENCE: ENGB-P01-001  
; CURRENT APPLICATION NUMBER: US/10/436,549  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: 60/379,626  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/393,233  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,235  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,211  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,280  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,197  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,223  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/430,948  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/433,319  
; PRIOR FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: 60/393,137  
; PRIOR FILING DATE: 2002-07-01  
; NUMBER OF SEQ ID NOS: 614  
; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 374  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Human  
US-10-436-549-374

Query Match 100.0%; Score 23; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
Db 1 DAHK 4

## RESULT 7

US-10-436-549-422  
; Sequence 422, Application US/10436549  
; Publication No. US20040038307A1  
; GENERAL INFORMATION:  
; APPLICANT: Lee, Frank D.

; APPLICANT: Meng, Dr. Xun  
; APPLICANT: Chan, John W.  
; APPLICANT: Zhang, Shengsheng  
; APPLICANT: Benkovic, Stephen J.  
; TITLE OF INVENTION: UNIQUE RECOGNITION SEQUENCES AND METHODS OF USE THEREOF IN  
; TITLE OF INVENTION: PROTEIN ANALYSIS  
; FILE REFERENCE: ENGE-P01-001  
; CURRENT APPLICATION NUMBER: US/10/436,549  
; CURRENT FILING DATE: 2003-05-12  
; PRIOR APPLICATION NUMBER: 60/379,626  
; PRIOR FILING DATE: 2002-05-10  
; PRIOR APPLICATION NUMBER: 60/393,233  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,235  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,211  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,280  
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; PRIOR APPLICATION NUMBER: 60/393,197  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/393,223  
; PRIOR FILING DATE: 2002-07-01  
; PRIOR APPLICATION NUMBER: 60/430,948  
; PRIOR FILING DATE: 2002-12-04  
; PRIOR APPLICATION NUMBER: 60/433,319  
; PRIOR FILING DATE: 2002-12-13  
; PRIOR APPLICATION NUMBER: 60/393,137  
; PRIOR FILING DATE: 2002-07-01  
; NUMBER OF SEQ ID NOS: 614  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 422  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Human  
US-10-436-549-422

Query Match 100.0%; Score 23; DB 12; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
Db 2 DAHK 5

RESULT 8  
US-10-205-110-24  
; Sequence 24, Application US/10205110  
; Publication No. US20030144471A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonassen, Ib  
; APPLICANT: Egel-Mitani, Michi  
; APPLICANT: Balschmidt, Per  
; APPLICANT: Markussen, Jan  
; APPLICANT: Diers, Ivan  
; APPLICANT: Kjeldsen, Thomas Borglum  
; TITLE OF INVENTION: Method for Making Acylated Polypeptides  
; FILE REFERENCE: 6289.200-US  
; CURRENT APPLICATION NUMBER: US/10/205,110  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: PA 2001 01141  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/310,793  
; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 24  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-205-110-24

US-10-205-110-24  
Query Match 100.0%; Score 23; DB 14; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
Db 2 DAHK 5

RESULT 9  
US-09-740-821-3  
; Sequence 3, Application US/09740821  
; Publication No. US20020006892A1  
; GENERAL INFORMATION:  
; APPLICANT: CARTER, Daniel C.  
; TITLE OF INVENTION: SERUM ALBUMIN COMPOSITIONS FOR USE IN CLEANSING OR DERMATOLOGICAL  
; FILE REFERENCE: P06652US01/BAS  
; CURRENT APPLICATION NUMBER: US/09/740,821  
; CURRENT FILING DATE: 2000-12-21  
; PRIOR APPLICATION NUMBER: 09/616,962  
; PRIOR FILING DATE: 2000-07-14  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-740-821-3

Query Match 100.0%; Score 23; DB 12; Length 6;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAHK 4  
Db 1 DAHK 4

RESULT 10  
US-10-205-110-47  
; Sequence 47, Application US/10205110  
; Publication No. US20030144471A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonassen, Ib  
; APPLICANT: Egel-Mitani, Michi  
; APPLICANT: Balschmidt, Per  
; APPLICANT: Markussen, Jan  
; APPLICANT: Diers, Ivan  
; APPLICANT: Kjeldsen, Thomas Borglum  
; TITLE OF INVENTION: Method for Making Acylated Polypeptides  
; FILE REFERENCE: 6289.200-US  
; CURRENT APPLICATION NUMBER: US/10/205,110  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: PA 2001 01141  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/310,793  
; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 47  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-205-110-47

Query Match 100.0%; Score 23; DB 14; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 1 DAKH 4  
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|  
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|  
Db 4 DAKH 7

## RESULT 11

US-10-393-992-2  
; Sequence 2, Application US/10393992  
; Publication No. US2004005645A1  
; GENERAL INFORMATION:  
; APPLICANT: Hanash, David G.  
; APPLICANT: Beer, David G.  
; APPLICANT: Knicker, Rork  
; APPLICANT: Hinderer, Robert  
; TITLE OF INVENTION: PROTEIN MARKERS FOR ESOPHAGEAL CANCER  
; FILE REFERENCE: 108140-00001  
; CURRENT APPLICATION NUMBER: US/10/393,992  
; CURRENT FILING DATE: 2003-03-24  
; PRIOR APPLICATION NUMBER: US/09/508,097  
; PRIOR FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US97/08656  
; PRIOR FILING DATE: 1997-05-29  
; PRIOR APPLICATION NUMBER: 60/018,659  
; PRIOR FILING DATE: 1996-05-30  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Sequence refers to 120, MW 25 kD, pH 5.8, albumin, cld

Query Match 100.0%; Score 23; DB 15; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAKH 4  
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|  
|  
|  
Db 1 DAKH 4

## RESULT 12

US-10-073-118-41  
; Sequence 41, Application US/10073118  
; Publication No. US2003005455A1  
; GENERAL INFORMATION:  
; APPLICANT: BECQUART, JEROME  
; TITLE OF INVENTION: ALBUMIN DERIVATIVES WITH THERAPEUTIC FUNCTIONS  
; FILE REFERENCE: 06832.1429-03  
; CURRENT APPLICATION NUMBER: US/10/073,118  
; CURRENT FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: 09/551,635  
; PRIOR FILING DATE: 2000-04-18  
; PRIOR APPLICATION NUMBER: 09/004,319  
; PRIOR FILING DATE: 1998-01-08  
; PRIOR APPLICATION NUMBER: 08/479,146  
; PRIOR FILING DATE: 1995-06-07  
; PRIOR APPLICATION NUMBER: 08/295,078  
; PRIOR FILING DATE: 1994-08-26  
; PRIOR APPLICATION NUMBER: 08/121,236  
; PRIOR FILING DATE: 1993-09-13  
; PRIOR APPLICATION NUMBER: 07/955,243  
; PRIOR FILING DATE: 1992-10-01  
; PRIOR APPLICATION NUMBER: 07/561,879  
; PRIOR FILING DATE: 1990-08-02  
; PRIOR APPLICATION NUMBER: FR 89 10480  
; PRIOR FILING DATE: 1989-08-03  
; NUMBER OF SEQ ID NOS: 41  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 41

; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-073-118-41

Query Match 100.0%; Score 23; DB 14; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAKH 4  
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|  
|  
|  
Db 2 DAKH 5

## RESULT 13

US-10-205-110-48  
; Sequence 48, Application US/10205110  
; Publication No. US20030144471A1  
; GENERAL INFORMATION:  
; APPLICANT: Jonassen, Ib  
; APPLICANT: Egel-Mitani, Michi  
; APPLICANT: Balschmidt, Per  
; APPLICANT: Markussen, Jan  
; APPLICANT: Diers, Ivan  
; APPLICANT: Kjeldsen, Thomas Borglum  
; TITLE OF INVENTION: Method for Making Acylated Polypeptides  
; FILE REFERENCE: 6289.200-US  
; CURRENT APPLICATION NUMBER: US/10/205,110  
; CURRENT FILING DATE: 2002-07-24  
; PRIOR APPLICATION NUMBER: PA 2001 01141  
; PRIOR FILING DATE: 2001-07-24  
; PRIOR APPLICATION NUMBER: 60/310,793  
; PRIOR FILING DATE: 2001-08-08  
; NUMBER OF SEQ ID NOS: 51  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 48  
; LENGTH: 9  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-205-110-48

Query Match 100.0%; Score 23; DB 14; Length 9;  
Best Local Similarity 100.0%; Pred. No. 1.2e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DAKH 4  
|  
|  
|  
|  
Db 6 DAKH 9

## RESULT 14

US-09-572-404B-2520  
; Sequence 2520, Application US/09572404B  
; Publication No. US20030078374A1  
; GENERAL INFORMATION:  
; APPLICANT: Proteom Ltd  
; TITLE OF INVENTION: Complementary peptide ligands from the human genome  
; FILE REFERENCE: Human patent  
; CURRENT APPLICATION NUMBER: US/09/572,404B  
; CURRENT FILING DATE: 2000-05-17  
; NUMBER OF SEQ ID NOS: 4203  
; SOFTWARE: ProPatent version 1.0  
; SEQ ID NO 2520  
; LENGTH: 10  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
; FEATURE:  
; OTHER INFORMATION: sequence located in SFR55 OR SRP40 OR HRS at 137-146 and may inte



; OTHER INFORMATION: with Sequence 2519 in this patent.

US-09-572-404B-2520

Query Match 100.0%; Score 23; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 Db 4 DAHK 7

RESULT 15

US-09-572-404B-2522

; Sequence 2522, Application US/09572404B

; Publication No. US20030078374A1

; GENERAL INFORMATION:

; APPLICANT: Proteom Ltd

; TITLE OF INVENTION: Complementary peptide ligands from the human genome

; FILE REFERENCE: Human patent

; CURRENT APPLICATION NUMBER: US/09/572,404B

; CURRENT FILING DATE: 2000-05-17

; NUMBER OF SEQ ID NOS: 4203

; SOFTWARE: ProtPatent version 1.0

; SEQ ID NO 2522

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapiens

; FEATURE:

; OTHER INFORMATION: sequence located in SFRS5 OR SRP40 OR HRS at 136-145 and may inte

; OTHER INFORMATION: with Sequence 2521 in this patent.

US-09-572-404B-2522

Query Match 100.0%; Score 23; DB 10; Length 10;  
 Best Local Similarity 100.0%; Pred. No. 97;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAHK 4  
 ||||  
 Db 5 DAHK 8

Search completed: September 9, 2004, 23:51:05  
 Job time : 142 secs